

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 4, 2004, 19:09:46 ; Search time 3463 seconds

(without alignments)
9624.832 Million cell updates/sec

Title: US-10-031-818b-1

Perfect score: 769

Sequence: 1 gggagctttttaaataacc.....ggtagcttttgagattccc 769

Scoring table: OLIGO NWC

Gapop 60.0 , Gapext 60.0

Searched: 3470272 segs, 2167151695 residues

Word size: 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenBank:*

1: gb_ba:*

2: gb_hgt:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_scs:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sls:*

28: em_un:*

29: em_vl:*

30: em_hgt_hum:*

31: em_hgt_inv:*

32: em_hgt_other:*

33: em_hgt_mus:*

34: em_hgt_pin:*

35: em_hgt_rod:*

36: em_hgt_mam:*

37: em_hgt_vrt:*

38: em_sy:*

39: em_hgt_hum:*

40: em_hgt_mus:*

41: em_hgt_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match %	Length	DB	ID	Description
1	769	100.0	769	6	ES2167	ES2167 Novel MITE-
2	769	100.0	769	6	AX078786	AX078786 Sequence
3	769	100.0	769	6	BD013409	BD013409 Transcript
4	769	100.0	1192	6	AX078788	AX078788 Sequence
5	769	100.0	1192	6	BD013411	BD013411 Transcript
6	769	100.0	1553	6	AX078799	AX078799 Sequence
7	769	100.0	1553	6	BD013422	BD013422 Transcript
8	769	100.0	7276	8	AB089813	AB089813 Dancus ca
9	158	20.5	158	6	ES2165	ES2165 Novel MITE-
10	158	20.5	158	6	ES2166	ES2166 Novel MITE-
11	158	20.5	158	6	AX078795	AX078795 Sequence
12	158	20.5	158	6	AX078796	AX078796 Sequence
13	158	20.5	158	6	BD013418	BD013418 Transcript
14	158	20.5	158	6	BD013419	BD013419 Transcript
15	112	14.6	769	6	ES2167	ES2167 Novel MITE-
16	112	14.6	769	6	AX078786	AX078786 Sequence
17	112	14.6	769	6	BD013409	BD013409 Transcript
18	112	14.6	1192	6	AX078788	AX078788 Sequence
19	112	14.6	1192	6	BD013411	BD013411 Transcript
20	112	14.6	1553	6	AX078799	AX078799 Sequence
21	112	14.6	1553	6	BD013422	BD013422 Transcript
22	112	14.6	7276	8	AB089813	AB089813 Dancus ca
23	31	4.0	185272	2	AC121394	AC121394 Rattus no
24	31	4.0	209878	2	AC121394	AC121394 Rattus no
25	31	4.0	209878	2	AC121318	AC121318 Rattus no
26	31	4.0	209878	2	AC121318	AC121318 Rattus no
27	30	3.9	158	6	ES2165	ES2165 Novel MITE-
28	30	3.9	158	6	AX078795	AX078795 Sequence
29	30	3.9	158	6	BD013418	BD013418 Transcript
30	30	3.9	620	11	BV067619	BV067619 S208P6733
31	30	3.9	745	8	AF009412	AF009412 Oryza sat
32	30	3.9	745	8	AF009412	AF009412 Oryza sat
33	30	3.9	110659	8	AP005691	AP005691 Oryza sat
34	30	3.9	110659	8	AP005691	AP005691 Oryza sat
35	30	3.9	113800	8	AC006567	AC006567 Arabidops
36	30	3.9	113800	8	AC006567	AC006567 Arabidops
37	30	3.9	113800	8	AC006567	AC006567 Arabidops
38	30	3.9	128411	5	AC107365	AC107365 Dancio rer
39	30	3.9	128411	5	AC107365	AC107365 Dancio rer
40	30	3.9	139056	2	AC141691	AC141691 Apis mell
41	30	3.9	139056	2	AC141691	AC141691 Apis mell
42	30	3.9	158971	2	AP004882	AP004882 Oryza sat
43	30	3.9	158971	2	AP004882	AP004882 Oryza sat
44	30	3.9	163710	3	AC023709	AC023709 Drosophila
45	30	3.9	163710	3	AC023709	AC023709 Drosophila

ALIGNMENTS

RESULT 1

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

JOURNAL

ES2167 Novel MITE-like factor. 769 bp DNA linear PAT 31-JAN-2002

ES2167 Novel MITE-like factor. 769 bp DNA linear PAT 31-JAN-2002

ES2167.1 GI:18629630

JP 2001029077-A/3.

unidentified

unclassified

1 (bases 1 to 769)
Koyanagi, M., Koseki, Y. and Koda, T.
Novel MITE-like factor
Patent: JP 2001029077-A 3 06-FEB-2001;
YOSHIIRO KOSEKI, SAN EI GEN FFI INC

COMMENT

OS Daucus carota L. cv. Kurodagosun (Carrot)
 PN JP 2001029077-A/3
 PD 06-FEB-2001
 PF 21-JUL-1999 JP 1999206316
 PR MIKIKO KOYANAGI, YOSHITIRO KOSEKI, TAKAOSHI KODA, PC
 CI2N15/09//A01H1/00, CI2N15/10, (CI2N15/09, CI2R1:91), CI2N15/00, PC
 CI2N5/00,
 PC (CI2N15/00, CI2R1:91)
 CC
 FT source 1. .769 Location/Qualifiers
 /organism="Daucus carota L. cv. Kurodagosun" FT

FEATURES

source
 1. .769
 /organism="unidentified"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"

ORIGIN

Query Match 100.0%; Score 769; DB 6; Length 769;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 769; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGATCTTTTAAATAATACCATCTGTAAATATTTTAAATAATACATCTTTT 60
 DB 1 GGGATCTTTTAAATAATACCATCTGTAAATATTTTAAATAATACATCTTTT 60
 QY 61 TCATGTTTAAATAATACCTTTTCATTAATTTTTCATAAATAATAGATTGCACT 120
 DB 61 TCATGTTTAAATAATACCTTTTCATTAATTTTTCATAAATAATAGATTGCACT 120
 QY 121 TTGGCAACTCATTTGCACTTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 180
 DB 121 TTGGCAACTCATTTGCACTTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 180
 QY 181 AAAGTTCAAATGAGTTGTAAAGTTGCAATGAGTTGCAAAAGTTGCAATAAAT 240
 DB 181 AAAGTTCAAATGAGTTGTAAAGTTGCAATGAGTTGCAAAAGTTGCAATAAAT 240
 QY 241 GGAAGTTGCAACAGTTGCAACAGTTGCAACAGTTGCAACAGTTGCAACAGTTG 300
 DB 241 GGAAGTTGCAACAGTTGCAACAGTTGCAACAGTTGCAACAGTTGCAACAGTTG 300
 QY 301 AAAAGTTGCAAAATGAGTTGCAAAATGAGTTGCAAAATGAGTTGCAAAATGAG 360
 DB 301 AAAAGTTGCAAAATGAGTTGCAAAATGAGTTGCAAAATGAGTTGCAAAATGAG 360
 QY 361 ATGGTGTCCCTGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 420
 DB 361 ATGGTGTCCCTGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 420
 QY 421 CAATGTAATCACTATATGCAATCACTATATGCAATCACTATATGCAATCACTAT 480
 DB 421 CAATGTAATCACTATATGCAATCACTATATGCAATCACTATATGCAATCACTAT 480
 QY 481 GTTTTGAATGTCAATTTTGAATGTCAATTTTGAATGTCAATTTTGAATGTCAAT 540
 DB 481 GTTTTGAATGTCAATTTTGAATGTCAATTTTGAATGTCAATTTTGAATGTCAAT 540
 QY 541 AATGATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTA 600
 DB 541 AATGATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTA 600
 QY 601 GAGGTTGCAACACGGCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 660
 DB 601 GAGGTTGCAACACGGCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 660
 QY 661 AGTATTTTGAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 720
 DB 661 AGTATTTTGAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 720

QY 721 TATTTTGAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 769
 DB 721 TATTTTGAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 769

RESULT 2

LOCUS AX078786 769 bp DNA linear PAT 22-FEB-2001
 DEFINITION Sequence 1 from Patent WO0105986.
 ACCSSION AX078786
 VERSION AX078786.1 GI:13158403
 KEYWORDS
 SOURCE Daucus carota (carrot)
 ORGANISM Daucus carota
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; campanulids; Apiales; Apiaceae; Apioidae; Scandiceae;
 Daucinae; Daucus.

REFERENCE
 AUTHORS Ozeki, Y., Oyanagi, M., Fukuda, T. and Koda, T. S.
 TITLE Mites-like element and transcriptional activation element
 JOURNAL Patent: WO 0105986-A1 25-JUN-2001;
 SAN-EI GEN F.R.I., INC. (JP) ; Ozeki, Yoshitiro (JP)

FEATURES
 source
 1. .769
 /organism="Daucus carota"
 /mol_type="unassigned DNA"
 /db_xref="taxon:4039"
 /note="L. cv. Kurodagosun"

ORIGIN

Query Match 100.0%; Score 769; DB 6; Length 769;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 769; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGATCTTTTAAATAATACCATCTGTAAATATTTTAAATAATACATCTTTT 60
 DB 1 GGGATCTTTTAAATAATACCATCTGTAAATATTTTAAATAATACATCTTTT 60
 QY 61 TCATGTTTAAATAATACCTTTTCATTAATTTTTCATAAATAATAGATTGCACT 120
 DB 61 TCATGTTTAAATAATACCTTTTCATTAATTTTTCATAAATAATAGATTGCACT 120
 QY 121 TTGGCAACTCATTTGCACTTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 180
 DB 121 TTGGCAACTCATTTGCACTTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 180
 QY 181 AAAGTTCAAATGAGTTGTAAAGTTGCAATGAGTTGCAAAAGTTGCAATAAAT 240
 DB 181 AAAGTTCAAATGAGTTGTAAAGTTGCAATGAGTTGCAAAAGTTGCAATAAAT 240
 QY 241 GGAAGTTGCAACAGTTGCAACAGTTGCAACAGTTGCAACAGTTGCAACAGTTG 300
 DB 241 GGAAGTTGCAACAGTTGCAACAGTTGCAACAGTTGCAACAGTTGCAACAGTTG 300
 QY 301 AAAAGTTGCAAAATGAGTTGCAAAATGAGTTGCAAAATGAGTTGCAAAATGAG 360
 DB 301 AAAAGTTGCAAAATGAGTTGCAAAATGAGTTGCAAAATGAGTTGCAAAATGAG 360
 QY 361 ATGGTGTCCCTGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 420
 DB 361 ATGGTGTCCCTGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 420
 QY 421 CAATGTAATCACTATATGCAATCACTATATGCAATCACTATATGCAATCACTAT 480
 DB 421 CAATGTAATCACTATATGCAATCACTATATGCAATCACTATATGCAATCACTAT 480
 QY 481 GTTTTGAATGTCAATTTTGAATGTCAATTTTGAATGTCAATTTTGAATGTCAAT 540
 DB 481 GTTTTGAATGTCAATTTTGAATGTCAATTTTGAATGTCAATTTTGAATGTCAAT 540
 QY 541 AATGATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTA 600
 DB 541 AATGATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTA 600

Db 541 AATGACATTCGAAACGTGAAATTCGAATTCAGCTGATATGAGTTGCAAA 600
Qy 601 GAGGTGGCAACGCGTGGCGCCGCTGTAGTTGCAAAATGAGTTGCAAAAGTTGCAAC 660
Db 601 GAGGTGGCAACGCGTGGCGCCGCTGTAGTTGCAAAATGAGTTGCAAAAGTTGCAAC 660
Qy 661 AGTATTTTGAAGAAAGATTTTATGAAAAGGTATTTTAAATAATTTCTGGAAGTGG 720
Db 661 AGTATTTTGAAGAAAGATTTTATGAAAAGGTATTTTAAATAATTTCTGGAAGTGG 720
Qy 721 TATTTTGAAGAAATGAAAGAAAGGTAGTTGTTTGTAGATTTC 769
Db 721 TATTTTGAAGAAATGAAAGAAAGGTAGTTGTTTGTAGATTTC 769

RESULT 3
BD013409
LOCUS BD013409 769 bp DNA linear PAT 27-AUG-2002
DEFINITION Transcriptional factor.
ACCESSION BD013409
VERSION BD013409.1 GI:22553723
KEYWORDS JP 2001086994-A/1.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 769)
AUTHORS Koyanagi, M., Fukuda, T., Ozeki, Y. and Koda, T.
TITLE Transcriptional factor
JOURNAL Patent: JP 2001086994-A 1 03-APR-2001;
YOSHIIRO OZEKI, SAN EI GEN FFI INC
OS Daucus carota L. cv. Kurodagosun (carrot)
PK JP 2001086994-A/1
PD 03-APR-2001
P2 12-JUN-2000 JP 2000175825
P3 MIKIKO KOYANAGI, TAKASHI FUKUDA, YOSHIIRO OZEKI, TAKATOSHI KODA
PC C12N15/09, A01H5/00//C12N5/10, C12N15/00, C12N5/00 CC
Transcriptional factor
FH Key Location/Qualifiers
FT source 1..769
/organism="Daucus carota L. cv. Kurodagosun FT
(carrot)";
Location/Qualifiers
1..769
/organism="unidentified";
/mol_type="genomic DNA";
/db_xref="taxon:32644"

ORIGIN
Query Match 100.0%; Score 769; DB 6; Length 769;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 769; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 GGGATCTTTTAAAAATACCCATCTGTAATAATTTTAAAAATCTACATCTTT 60
Qy 1 GGGATCTTTTAAAAATACCCATCTGTAATAATTTTAAAAATCTACATCTTT 60
Db 1 GGGATCTTTTAAAAATACCCATCTGTAATAATTTTAAAAATCTACATCTTT 60
Qy 61 TCAATGTTTTTAAAAATACCTTTTCAATAATTTTCTTCAAAAATAGATTGCAACT 120
Db 61 TCAATGTTTTTAAAAATACCTTTTCAATAATTTTCTTCAAAAATAGATTGCAACT 120
Qy 121 TTGCAACCTCATTTGCAACCTTTGGCGGCGAGCCGTAAAGTTGCCAGTGAAGTTGCA 180
Db 121 TTGCAACCTCATTTGCAACCTTTGGCGGCGAGCCGTAAAGTTGCCAGTGAAGTTGCA 180
Qy 181 AAAGTTGCAATGAGTTGTAAAGTTGCAAAATGAGTTGCAAAAGTTGCAAAATGAAAT 240
Db 181 AAAGTTGCAATGAGTTGTAAAGTTGCAAAATGAGTTGCAAAAGTTGCAAAATGAAAT 240
Qy 241 GGAAGTTGCAACAGTTGCAACTGCAATTTGCAACTAGTTCAACTGAAATCTGAAGTTGC 300
Db 241 GGAAGTTGCAACAGTTGCAACTGCAATTTGCAACTAGTTCAACTGAAATCTGAAGTTGC 300
Qy 301 AAAAGTTGCAATGAGTTGCAACTGAAATGCAACTGTAAGTAAACAAGAGTGT 360

Db 301 AAAAGTTGCAATGAGTTGCAACTGAAATGCAACTGTAAGTAAACAAGAGTGT 360
Qy 361 ATGTGTGCCCCCTGGCGGCGCCGCTGTAGATTACATAGAAATCACTGAAATGCAATATAG 420
Db 361 ATGTGTGCCCCCTGGCGGCGCCGCTGTAGATTACATAGAAATCACTGAAATGCAATATAG 420
Qy 421 CAAGTGAATACAACTATATAGCAATCATATATAGCAATTTACAAATCTGATTTCAAGTTGCA 480
Db 421 CAAGTGAATACAACTATATAGCAATCATATATAGCAATTTACAAATCTGATTTCAAGTTGCA 480
Qy 481 GTTTTGAATGTCAATTTTGAATATGATATATATATATATATATATATATATATATATATAT 540
Db 481 GTTTTGAATGTCAATTTTGAATATGATATATATATATATATATATATATATATATATATAT 540
Qy 541 AATGACATTCGAAACGTGAAATTCGAATTCAGCTGATATGAGTTGCAAA 600
Db 541 AATGACATTCGAAACGTGAAATTCGAATTCAGCTGATATGAGTTGCAAA 600
Qy 601 GAGGTGGCAACGCGTGGCGCCGCTGTAGTTGCAAAATGAGTTGCAAAAGTTGCAAC 660
Db 601 GAGGTGGCAACGCGTGGCGCCGCTGTAGTTGCAAAATGAGTTGCAAAAGTTGCAAC 660
Qy 661 AGTATTTTGAAGAAAGATTTTATGAAAAGGTATTTTAAATAATTTCTGGAAGTGG 720
Db 661 AGTATTTTGAAGAAAGATTTTATGAAAAGGTATTTTAAATAATTTCTGGAAGTGG 720
Qy 721 TATTTTGAAGAAATGAAAGAAAGGTAGTTGTTTGTAGATTTC 769
Db 721 TATTTTGAAGAAATGAAAGAAAGGTAGTTGTTTGTAGATTTC 769

RESULT 4
AX078788
LOCUS AX078788 1192 bp DNA linear PAT 22-FEB-2001
DEFINITION Sequence 3 from Patent WO0105986.
ACCESSION AX078788
VERSION AX078788.1 GI:1158405
KEYWORDS
SOURCE Daucus carota (carrot)
ORGANISM Daucus carota
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; Campanulids; Apiales; Apiaceae; Apioidae; Scandiceae;
Daucineae; Daucus.
REFERENCE 1
AUTHORS Ozeki, Y., Oyanagi, M., Fukuda, T. and Koda, T.S.
TITLE Mites-like element and transcriptional activation element
JOURNAL Patent: WO 0105986-A 3 25-JAN-2001;
SAN-EI GEN F.F.I., INC. (JP) ; Ozeki, Yoshihiro (JP)
FEATURES
source Location/Qualifiers
1..1192
/organism="Daucus carota";
/mol_type="unassigned DNA";
/db_xref="taxon:4039";
/note="L. cv. Kurodagosun"

ORIGIN
Query Match 100.0%; Score 769; DB 6; Length 1192;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 769; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 GGGATCTTTTAAAAATACCCATCTGTAATAATTTTAAAAATCTACATCTTT 60
Qy 1 GGGATCTTTTAAAAATACCCATCTGTAATAATTTTAAAAATCTACATCTTT 60
Db 399 GGGATCTTTTAAAAATACCCATCTGTAATAATTTTAAAAATCTACATCTTT 458
Qy 61 TCAATGTTTTTAAAAATACCTTTTCAATAATTTTCTTCAAAAATAGATTGCAACT 120
Db 61 TCAATGTTTTTAAAAATACCTTTTCAATAATTTTCTTCAAAAATAGATTGCAACT 120
Qy 121 TTGCAACCTCATTTGCAACCTTTGGCGGCGAGCCGTAAAGTTGCCAGTGAAGTTGCA 180
Db 121 TTGCAACCTCATTTGCAACCTTTGGCGGCGAGCCGTAAAGTTGCCAGTGAAGTTGCA 180
Qy 181 AAAGTTGCAATGAGTTGTAAAGTTGCAAAATGAGTTGCAAAAGTTGCAAAATGAAAT 240
Db 181 AAAGTTGCAATGAGTTGTAAAGTTGCAAAATGAGTTGCAAAAGTTGCAAAATGAAAT 240
Qy 241 GGAAGTTGCAACAGTTGCAACTGCAATTTGCAACTAGTTCAACTGAAATCTGAAGTTGC 300
Db 241 GGAAGTTGCAACAGTTGCAACTGCAATTTGCAACTAGTTCAACTGAAATCTGAAGTTGC 300
Qy 301 AAAAGTTGCAATGAGTTGCAACTGAAATGCAACTGTAAGTAAACAAGAGTGT 360

```

/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

```

REFERENCE

1. Dancinae, Daucus.

ORGANISM

DAUCUS carota (carrot)

SOURCES

DAUCUS carota

Euarrysta, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Euarysta, Viridiplantae; Streptophyta; eudicotyledons; core eudicots; Spermatophytes; Magnoliophyta; eucoiclydoms; core eudicots; asterids; Campanulids; Apiales; Apiaceae; Apioidae; Scandiceae; Dancinae, Daucus.

AUTHORS Ozeki,Y., Oyamagi,M., Fukuda,T. and Koda,T.S.
 TITLE Mites-like element and transcriptional activation element
 JOURNAL Patent: WO 0105986-A 14 25-JAN-2001;
 SAN-EI GEN F.F.I., INC. (JPN) ; Ozeki, Yoshihiro (JP)

FEATURES Location/Qualifiers
 source 1..1553

/organism="Daucus carota"
 /mol_type="unassigned DNA"
 /db_xref="taxon:4039"
 /note="L.cv. Kurodagosun"

ORIGIN

Query Match 100.0%; Score 769; DB 6; Length 1553;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 769; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 GGGATCTTTTAAAAATACCACATCTGTAATAATATTTTAAAAATACACATCTTTT 60
DB 766 GGGATCTTTTAAAAATACCACATCTGTAATAATATTTTAAAAATACACATCTTTT 825
QY 61 TCATGCTTTTAAAAATACCTTTTCATTAATTTTTCACAAAAATACGATTTCACACT 120
DB 826 TCATGCTTTTAAAAATACCTTTTCATTAATTTTTCACAAAAATACGATTTCACACT 885
QY 121 TTTCGACCTCATTTTGCACCTTTGGGCGCGCAGCCGTAAAGTTGCCAGTGAAGTTGA 180
DB 886 TTTCGACCTCATTTTGCACCTTTGGGCGCGCAGCCGTAAAGTTGCCAGTGAAGTTGA 945
QY 181 AAAGTGCAAATGAGTTTGTAAAGTTGCAAAATGAGTTGCAAAAGTTGCAATAAAAT 240
DB 946 AAAGTGCAAATGAGTTTGTAAAGTTGCAAAATGAGTTGCAAAAGTTGCAATAAAAT 1005
QY 241 GGAAGTTGCAACAGTTGCACTGCAATGTCACCTGTAACCTGTAAGTTGC 300
DB 1006 GGAAGTTGCAACAGTTGCACTGCAATGTCACCTGTAACCTGTAAGTTGC 1065
QY 301 AAAAGTTGCAAAATGAGTTGCACTGCAATGTCACCTGTAAGTTGCAAAAGTTGCA 360
DB 1066 AAAAGTTGCAAAATGAGTTGCACTGCAATGTCACCTGTAAGTTGCAAAAGTTGCA 1125
QY 361 ATGCTGTGCCCCCTGGCGGCGCGTGAATTAACAATGAAATCAATGCAATGCAATCATG 420
DB 1126 ATGCTGTGCCCCCTGGCGGCGCGTGAATTAACAATGAAATCAATGCAATGCAATCATG 1185
QY 421 CAACGTAAATCAACTATATGCAATCAATATGCAATTAACAATCCGATTTGAAGTTCA 480
DB 1186 CAACGTAAATCAACTATATGCAATCAATATGCAATTAACAATCCGATTTGAAGTTCA 1245
QY 481 GTTTTGAATGTCATTTTGAATTCGATATATATATATATATATATATATATATATATG 540
DB 1246 GTTTTGAATGTCATTTTGAATTCGATATATATATATATATATATATATATATATATG 1305
QY 541 AATGCAATTCGAAATTCGAAATTCGAAATTCGAAATTCGAAATTCGAAATTCGAAATTC 600
DB 1306 AATGCAATTCGAAATTCGAAATTCGAAATTCGAAATTCGAAATTCGAAATTCGAAATTC 1365
QY 601 GAGTTGCAACAACGCGTGGCGCGCTGATGTTGCAAAATGAGTTGCAAAAGTTGCAAA 660
DB 1366 GAGTTGCAACAACGCGTGGCGCGCTGATGTTGCAAAATGAGTTGCAAAAGTTGCAAA 1425
QY 661 AGTATTTTGGAAAAAGATTTTATGAAAAAGTATTTTAAAAAATATCTGGAAGTTG 720
DB 1426 AGTATTTTGGAAAAAGATTTTATGAAAAAGTATTTTAAAAAATATCTGGAAGTTG 1485
QY 721 TATTTTGAACAATTAAGAAAAAGGTAGTTTGTAGATTTTCCC 769
DB 1486 TATTTTGAACAATTAAGAAAAAGGTAGTTTGTAGATTTTCCC 1534

```

RESULT 7
 BD013422
 LOCUS BD013422 1553 bp DNA linear PAT 27-AUG-2002
 DEFINITION Transcriptional factor.

ACCESSION BD013422
 VERSION BD013422.1 GI:22553736
 KEYWORDS JP 2001086994-A/14.
 SOURCE unidentified
 ORGANISM unidentified

REFERENCE 1 (bases 1 to 1553)
 Koyamagi,M., Fukuda,T., Ozeki,Y. and Koda,T.
 TITLE Transcriptional factor
 JOURNAL Patent: JP 2001086994-A 14 03-APR-2001;
 YOSHIHIRO OZEKI,SAN EI GEN FFI INC

COMMENT OS Daucus carota L.cv. Kurodagosun (carrot)
 PN JP 2001086994-A/14
 PD 03-APR-2001
 PF 12-JUN-2000 JP 2000175825
 PI MIKIRO KOYAMAGI,TAKASHI FUKUDA,YOSHIHIRO OZEKI,TAKATOSHI KODA
 PC C12N15/09,A01H5/00/C12N5/10,C12N15/00,C12N5/00 CC
 TRANSCRIPTIONAL FACTOR
 FH Key
 FT source 1..1553
 Location/Qualifiers
 (carrot)'
 1..1553
 /organism="Daucus carota L.cv. Kurodagosun"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"

FEATURES

source

ORIGIN

Query Match 100.0%; Score 769; DB 6; Length 1553;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 769; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 GGGATCTTTTAAAAATACCACATCTGTAATAATATTTTAAAAATACACATCTTTT 60
DB 766 GGGATCTTTTAAAAATACCACATCTGTAATAATATTTTAAAAATACACATCTTTT 825
QY 61 TCATGCTTTTAAAAATACCTTTTCATTAATTTTTCACAAAAATACGATTTCACACT 120
DB 826 TCATGCTTTTAAAAATACCTTTTCATTAATTTTTCACAAAAATACGATTTCACACT 885
QY 121 TTTCGACCTCATTTTGCACCTTTGGGCGCGCAGCCGTAAAGTTGCCAGTGAAGTTGA 180
DB 886 TTTCGACCTCATTTTGCACCTTTGGGCGCGCAGCCGTAAAGTTGCCAGTGAAGTTGA 945
QY 181 AAAGTGCAAATGAGTTTGTAAAGTTGCAAAATGAGTTGCAAAAGTTGCAATAAAAT 240
DB 946 AAAGTGCAAATGAGTTTGTAAAGTTGCAAAATGAGTTGCAAAAGTTGCAATAAAAT 1005
QY 241 GGAAGTTGCAACAGTTGCACTGCAATGTCACCTGTAACCTGTAAGTTGC 300
DB 1006 GGAAGTTGCAACAGTTGCACTGCAATGTCACCTGTAACCTGTAAGTTGC 1065
QY 301 AAAAGTTGCAAAATGAGTTGCACTGCAATGTCACCTGTAAGTTGCAAAAGTTGCA 360
DB 1066 AAAAGTTGCAAAATGAGTTGCACTGCAATGTCACCTGTAAGTTGCAAAAGTTGCA 1125
QY 361 ATGCTGTGCCCCCTGGCGGCGCGTGAATTAACAATGAAATCAATGCAATGCAATCATG 420
DB 1126 ATGCTGTGCCCCCTGGCGGCGCGTGAATTAACAATGAAATCAATGCAATGCAATCATG 1185
QY 421 CAACGTAAATCAACTATATGCAATCAATATGCAATTAACAATCCGATTTGAAGTTCA 480
DB 1186 CAACGTAAATCAACTATATGCAATCAATATGCAATTAACAATCCGATTTGAAGTTCA 1245
QY 481 GTTTTGAATGTCATTTTGAATTCGATATATATATATATATATATATATATATATATG 540
DB 1246 GTTTTGAATGTCATTTTGAATTCGATATATATATATATATATATATATATATATATG 1305
QY 541 AATGCAATTCGAAATTCGAAATTCGAAATTCGAAATTCGAAATTCGAAATTCGAAATTC 600
DB 1306 AATGCAATTCGAAATTCGAAATTCGAAATTCGAAATTCGAAATTCGAAATTCGAAATTC 1365

```

QY 601 GAGGTTCACACGCGCTGCGCGCCCTGTAGTTGCAATGAGTTGCAAAAGTTGCAAC 660
 DB 1366 GAGGTTCACACGCGCTGCGCGCCCTGTAGTTGCAATGAGTTGCAAAAGTTGCAAC 1425
 QY 661 AGTATTTTGAATAAAGATTTTATGAAAAGGTATTTTAAATAATCTCGAAGGTAG 720
 DB 1426 AGTATTTTGAATAAAGATTTTATGAAAAGGTATTTTAAATAATCTCGAAGGTAG 1485
 QY 721 TATTTTGAATAAAGATTTTATGAAAAGGTATTTTATGATTTCC 769
 DB 1486 TATTTTGAATAAAGATTTTATGAAAAGGTATTTTATGATTTCC 1534
 RESULT 8
 LOCUS AB089813 7276 bp DNA linear JUN 11-FEB-2003
 DEFINITION Daucus carota gdcPAL3 gene for phenylalanine ammonia-lyase,
 complete cds.
 ACCESSION AB089813
 VERSION AB089813.1 GI:28316385
 KEYWORDS
 ORGANISM Daucus carota (carrot)
 Daucus carota
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; campanulids; Apiales; Apiaceae; Apioideae; Scandiceae;
 Daucineae; Daucus.
 REFERENCE 1
 AUTHORS Ozeki,Y., Chikagawa,Y., Kimura,S., Sch,H., Maeda,K.,
 Yamanashi,M., Kato,M., Akimoto,H., Oyanagi,M., Fukuda,T.,
 Kodai,T., Itoh,Y., Yamada,A., Ueno,H. and Takeda,J.
 TITLE Purative cis-elements in the promoter region of phenylalanine
 ammonia-lyase gene of carrot involved in anthocyanin biosynthetic
 pathway
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 7276)
 AUTHORS Ozeki,Y., Chikagawa,Y., Kimura,S., Maeda,K., Oyanagi,M., Fukuda,T.,
 Kodai,T., Itoh,Y., Yamada,A. and Takeda,J.
 TITLE Direct Submision
 JOURNAL Submitted (13-AUG-2002) Yoshihiro Ozeki, Tokyo University of
 Agriculture and Technology, Department of Biotechnology, Naka-chou
 2-24-16, Koganei, Tokyo 184-8588, Japan
 (E-mail:ozeki@cc.tuat.ac.jp, Tel:81-42-388-7239,
 Fax:81-42-388-7239)
 FEATURES
 source location/Qualifiers
 1..7276
 /organism="Daucus carota"
 /mol_type="genomic DNA"
 /cultiivar="Kurodagosen"
 /db_xref="taxon:4039"
 /note="cultured cells"
 2510..2514
 2540..2705
 join(2706..3100,4423..6175)
 /gene="gdcPAL3"
 /name="gdcPAL3"
 /EC_number="4.3.1.5"
 /codon_start=1
 /evidence=experimental
 /product="phenylalanine ammonia-lyase"
 /protein_id="AAC56977.1"
 /db_xref="GI:28316385"
 /translation="MAITNGHENGNCYDLECKKEDPELSWVAABAKGSHLEBYKRN
 VARYKPVVKLGSTLTISQVAISADDSVXVLELSBAAGVASSDWMSWANG
 TDSYGVTTGFGATSHRRTQGAALQKELIRPLNAGIFGSGAAGNPLPSATRAAML
 VRINTLQVSGIGFEBILKATKFLNENITPCLPURGITASGDLVPLSYIAGLTGR
 PNRKAVGPTGTLSPBEAFKAGYEGGFFELQPKKGAALVNGTAVGSGMAMVLEAN
 ILAVLAETMAISPAVMOGKPEFTDLTHLKHKHPGOEBAALVEHETLDSAAVYKAA
 KLEHMDPLQKPKORALRTSPQWLGROIETVRSSTGTEIEEINSVNDPLIDVSRK
 AIHGGNGPTPIGVSMNTRILALAIQGLTANRQSELVNDYNNGLSNLSGGNPNL
 DYFGKALIMASVCSDELQFLANFVTHVQABORHODVNSGLISNRKSEAVEILK
 LMSITFLVGLCOALDLRLHENLAKSVKNTVSQVAKRVLTVNGELHPSRPECIDL
 TATA signal
 5'UTR
 gene
 CDS

Query Match 100.0%; Score 769; DB 8; Length 7276;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 769; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 ORIGIN
 intron
 polyA_signal
 /gene="gdcPAL3"
 6320..6325
 RVDREYIPAYIDDPCSATYELMKURELVEHALNNGDKERNLSTSIPOKIAFEDE
 EKALPEVESARAIVESGNPAIPNRIKERSPLVKVFVEEISTELETGERKTSRGE
 EPDKVFLPMKGEIIDLPLEELGSMWGAFLPIC"
 3101..4422
 1 GGGATCTTTTAAATAACCATCTGTAATAATTTTAAATAATCTGTAACCTTTT 60
 DB 1383 GGGATCTTTTAAATAACCATCTGTAATAATTTTAAATAATCTGTAACCTTTT 1442
 QY 61 TCATTTGTTTAAATAACCTTTTCAATTAATTTTAAATAATCTGTAACCTTTT 120
 DB 1443 TCATTTGTTTAAATAACCTTTTCAATTAATTTTAAATAATCTGTAACCTTTT 1502
 QY 121 TTGCAACTCATTTGCAACCTTGGCGCGCGACCCGTAATAAGTTGCCAGTTCGA 180
 DB 1503 TTGCAACTCATTTGCAACCTTGGCGCGCGACCCGTAATAAGTTGCCAGTTCGA 1562
 QY 181 AAGTTGCAATGAGTTGTAAAGTTGCAATGAGTTGCAATGAGTTGCAATTAAT 240
 DB 1563 AAGTTGCAATGAGTTGTAAAGTTGCAATGAGTTGCAATGAGTTGCAATTAAT 1622
 QY 241 GGAAGTTGCAACGTTGCAACGTTGCAACGTTGCAACGTTGCAACGTTGCAACGTTG 300
 DB 1623 GGAAGTTGCAACGTTGCAACGTTGCAACGTTGCAACGTTGCAACGTTGCAACGTTG 1682
 QY 301 AAAAGTTGCAATGAGTTGTAAAGTTGCAATGAGTTGCAATGAGTTGCAATTAAT 360
 DB 1683 AAAAGTTGCAATGAGTTGTAAAGTTGCAATGAGTTGCAATGAGTTGCAATTAAT 1742
 QY 361 ATGGTGCCCTCGCGCGCGCGCTGTAGTTTACATTAATCAATCAATCAATCATATG 420
 DB 1743 ATGGTGCCCTCGCGCGCGCGCTGTAGTTTACATTAATCAATCAATCAATCATATG 1802
 QY 421 CAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 480
 DB 1803 CAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1862
 QY 481 GTTTGCAATGATTTGCAATGATTTGCAATGATTTGCAATGATTTGCAATGATTTGCA 540
 DB 1863 GTTTGCAATGATTTGCAATGATTTGCAATGATTTGCAATGATTTGCAATGATTTGCA 1922
 QY 541 AATGCACTTGCAAACTGCAAACTGCAAACTGCAAACTGCAAACTGCAAACTGCAAACT 600
 DB 1923 AATGCACTTGCAAACTGCAAACTGCAAACTGCAAACTGCAAACTGCAAACTGCAAACT 1982
 QY 601 GAGGTTCACACGCGCTGCGCGCCCTGTAGTTGCAATGAGTTGCAAAAGTTGCAAC 660
 DB 1983 GAGGTTCACACGCGCTGCGCGCCCTGTAGTTGCAATGAGTTGCAAAAGTTGCAAC 2042
 QY 661 AGTATTTTGAATAAAGATTTTATGAAAAGGTATTTTAAATAATCTCGAAGGTAG 720
 DB 2043 AGTATTTTGAATAAAGATTTTATGAAAAGGTATTTTAAATAATCTCGAAGGTAG 2102
 QY 721 TATTTTGAATAAAGATTTTATGAAAAGGTATTTTATGATTTCC 769
 DB 2103 TATTTTGAATAAAGATTTTATGAAAAGGTATTTTATGATTTCC 2151
 RESULT 9
 LOCUS B52165 158 bp DNA linear PAT 31-JAN-2002
 DEFINITION Novel MTR-1like factor.
 ACCESSION B52165
 VERSION B52165.1 GI:18629628
 KEYWORDS UP 2001029077-A/1.
 SOURCE unidentified

ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 158)
AUTHORS Koyanagi, M., Koseki, Y. and Koda, T.
TITLE Novel MITE-like factor
JOURNAL Patent: JP 2001029077-A 1 06-FEB-2001;
YOSHIIRO KOSEKI, SAN EI GEN FFI INC
OS Daucus carota L. cv. Kurodagosun (Carrot)
PD JP 2001029077-A/1
PF 06-FEB-2001
PR 21-JUL-1999 JP 1999206316

FEATURES
source Location/Qualifiers
FT 1.158
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN
Query Match 20.5%; Score 158; DB 6; Length 158;
Best Local Similarity 100.0%; Pred. No. 9.6e-71;
Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

LOCUS E52166 158 bp DNA linear PAT 31-JAN-2002
DEFINITION Novel MITE-like factor.
ACCESSION E52166
VERSION E52166.1 GI:18629629
KEYWORDS JP 2001029077-A/2.
SOURCE unidentified
ORGANISM unidentified

REFERENCE 1 (bases 1 to 158)
AUTHORS Koyanagi, M., Koseki, Y. and Koda, T.
TITLE Novel MITE-like factor
JOURNAL Patent: JP 2001029077-A 2 06-FEB-2001;
YOSHIIRO KOSEKI, SAN EI GEN FFI INC
OS Daucus carota L. cv. Kurodagosun (Carrot)
PD JP 2001029077-A/2
PF 06-FEB-2001
PR 21-JUL-1999 JP 1999206316

COMMENT
P1 MIKIKO KOYANAGI, YOSHIIRO KOSEKI, TAKAOSHI KODA PC
C12N15/09//A01H1/00, C12N5/10, (C12N15/09, C12R1:91), C12N15/00, PC
C12N5/00,
PC (C12N15/00, C12R1:91)
CC
FH Key Location/Qualifiers
FT source 1.158
/organism="Daucus carota L. cv. Kurodagosun" FT

1 GGGATCTTTTAAAAATACCCATCTGTAATATTTTAAAAATACCACTTTT 60
Db 1 GGGATCTTTTAAAAATACCCATCTGTAATATTTTAAAAATACCACTTTT 60
Qy 61 TCATGTCTTTTAAAAATACCTTTTCATTAATTTTTCACAAAATACGATTGCACT 120
Db 61 TCATGTCTTTTAAAAATACCTTTTCATTAATTTTTCACAAAATACGATTGCACT 120
Qy 121 TTGCAACCTCATTTGCAACCTTTGGCGCGCGACCGCT 158
Db 121 TTGCAACCTCATTTGCAACCTTTGGCGCGCGACCGCT 158

FEATURES
source Location/Qualifiers
FT 1.158
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN
Query Match 20.5%; Score 158; DB 6; Length 158;
Best Local Similarity 100.0%; Pred. No. 9.6e-71;
Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

LOCUS AX078795 158 bp DNA linear PAT 22-FEB-2001
DEFINITION Sequence 10 from Patent WO0105986.
ACCESSION AX078795
VERSION AX078795.1 GI:13158412
KEYWORDS
SOURCE Daucus carota (carrot)
ORGANISM Daucus carota
Buxaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Apiales; Apiaceae; Apioidae; Scandideae;
Daucinae; Daucus.
REFERENCE 1
AUTHORS Ozeki, Y., Oyanagi, M., Fukuda, T. and Koda, T. S.
TITLE Mites-like element and transcriptional activation element
JOURNAL Patent: WO 0105986-A 10 25-JAN-2001;
SAN-EI GEN F.F.I., INC. (JP) ; Ozeki, Yoshihiro (JP)
LOCATION/Qualifiers
source 1.158
/organism="Daucus carota"
/mol_type="unassigned DNA"
/db_xref="taxon:4039"
/note="L. cv. Kurodagosun"

ORIGIN
Query Match 20.5%; Score 158; DB 6; Length 158;
Best Local Similarity 100.0%; Pred. No. 9.6e-71;
Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

LOCUS AX078796 158 bp DNA linear PAT 22-FEB-2001
DEFINITION Sequence 11 from Patent WO0105986.
ACCESSION AX078796

1 GGGATCTTTTAAAAATACCCATCTGTAATATTTTAAAAATACCACTTTT 60
Db 1 GGGATCTTTTAAAAATACCCATCTGTAATATTTTAAAAATACCACTTTT 60
Qy 61 TCATGTCTTTTAAAAATACCTTTTCATTAATTTTTCACAAAATACGATTGCACT 120
Db 61 TCATGTCTTTTAAAAATACCTTTTCATTAATTTTTCACAAAATACGATTGCACT 120
Qy 121 TTGCAACCTCATTTGCAACCTTTGGCGCGCGACCGCT 158
Db 121 TTGCAACCTCATTTGCAACCTTTGGCGCGCGACCGCT 158

VERSION AX078796.1 GI:13158413
KEYWORDS
SOURCE Daucus carota (carrot)
ORGANISM Daucus carota
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Apiales; Apiaceae; Apioidae; Scandiceae;
Daucinae; Daucus.
REFERENCE 1
AUTHORS Ozeki,Y., Oyanagi,M., Fukuda,T. and Koda,T.S.
TITLE Mites-like element and transcriptional activation element
JOURNAL Patent: WO 0105986-A 11 25-JAN-2001;
SAN-EI GEN F.F.I., INC. (JP) ; Ozeki, Yoshihiro (JP)
FEATURES
Source Location/Qualifiers
1..158
/organism="Daucus carota"
/mol_type="unassigned DNA"
/db_xref="taxon:4039"
/note="L.cv.Kurodagosun"

ORIGIN

Query Match 20.5%; Score 158; DB 6; Length 158;
Best Local Similarity 100.0%; Pred. No. 9.6e-71;
Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 612 ACGGCTGGCGCCCTGTAGTTCGAATGAGTTCGAAGAAGTTCGAACAGTATTTTGA 671
Db 1 ACGGCTGGCGCCCTGTAGTTCGAATGAGTTCGAAGAAGTTCGAACAGTATTTTGA 60
Qy 672 AAAAAAGTTTATGAAAAAGTATTTTAAATAATTCGAAAGTATTTTGA 731
Db 61 AAAAAAGTTTATGAAAAAGTATTTTAAATAATTCGAAAGTATTTTGA 120
Qy 732 ACAATTAAGAAAAAGTAGTAGTTTGTAGATTTCC 769
Db 121 ACAATTAAGAAAAAGTAGTAGTTTGTAGATTTCC 158

RESULT 13
BD013418
LOCUS BD013418 158 bp DNA linear PAT 27-AUG-2002
DEFINITION Transcriptional factor.
ACCESSION BD013418.1 GI:22553732
VERSION JP 2001086994-A/10.
KEYWORDS unclassified
SOURCE unclassified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 158)
AUTHORS Koyanagi,M., Fukuda,T., Ozeki,Y. and Koda,T.
TITLE Transcriptional factor
JOURNAL Patent: JP 2001086994-A 10 03-APR-2001;
YOSHIHIRO OZEKI,SAN EI GEN FFI INC
OS Daucus carota L.cv.Kurodagosun (carrot)
PN JP 2001086994-A/10
PD 03-APR-2001
PI 12-JUN-2000 JP 2000175825
PC C12N15/09,A01H5/00//C12N5/10,C12N15/00,C12N5/00 CC
Transcriptional factor
FH Key Location/Qualifiers
FT source 1..158
/organism="Daucus carota L.cv.Kurodagosun FT
(carrot)";

FEATURES

Source Location/Qualifiers
1..158
/organism="unclassified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN

Query Match 20.5%; Score 158; DB 6; Length 158;
Best Local Similarity 100.0%; Pred. No. 9.6e-71;

Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGATCTTTTAAAAAACCATCTGTAAATATTTTAAAAATACATCATCTTTT 60
Db 1 GGGATCTTTTAAAAAACCATCTGTAAATATTTTAAAAATACATCATCTTTT 60
Qy 61 TCAATGTTTAAAAATACCTTTTCATTAATTTTTCGAAAAATACATTTGCACT 120
Db 61 TCAATGTTTAAAAATACCTTTTCATTAATTTTTCGAAAAATACATTTGCACT 120
Qy 121 TTTCGAACCTCATTTGCAACCTTGGCGGCGACCGT 158
Db 121 TTTCGAACCTCATTTGCAACCTTGGCGGCGACCGT 158

RESULT 14
BD013419
LOCUS BD013419 158 bp DNA linear PAT 27-AUG-2002
DEFINITION Transcriptional factor.
ACCESSION BD013419.1 GI:22553733
VERSION JP 2001086994-A/11.
KEYWORDS unclassified
SOURCE unclassified
ORGANISM unclassified

REFERENCE 1 (bases 1 to 158)
AUTHORS Koyanagi,M., Fukuda,T., Ozeki,Y. and Koda,T.
TITLE Transcriptional factor
JOURNAL Patent: JP 2001086994-A 11 03-APR-2001;
YOSHIHIRO OZEKI,SAN EI GEN FFI INC
OS Daucus carota L.cv.Kurodagosun (carrot)
PN JP 2001086994-A/11
PD 03-APR-2001
PI 12-JUN-2000 JP 2000175825
PC C12N15/09,A01H5/00//C12N5/10,C12N15/00,C12N5/00 CC
Transcriptional factor
FH Key Location/Qualifiers
FT source 1..158
/organism="Daucus carota L.cv.Kurodagosun FT
(carrot)";

FEATURES

Source Location/Qualifiers
1..158
/organism="unclassified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN

Query Match 20.5%; Score 158; DB 6; Length 158;
Best Local Similarity 100.0%; Pred. No. 9.6e-71;
Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 612 ACGGCTGGCGCCCTGTAGTTCGAATGAGTTCGAAGAAGTTCGAACAGTATTTTGA 671
Db 1 ACGGCTGGCGCCCTGTAGTTCGAATGAGTTCGAAGAAGTTCGAACAGTATTTTGA 60
Qy 672 AAAAAAGTTTATGAAAAAGTATTTTAAATAATTCGAAAGTATTTTGA 731
Db 61 AAAAAAGTTTATGAAAAAGTATTTTAAATAATTCGAAAGTATTTTGA 120
Qy 732 ACAATTAAGAAAAAGTAGTAGTTTGTAGATTTCC 769
Db 121 ACAATTAAGAAAAAGTAGTAGTTTGTAGATTTCC 158

RESULT 15
E52167/C
LOCUS E52167 769 bp DNA linear PAT 31-JAN-2002
DEFINITION Novel MITE-like factor.
ACCESSION E52167
VERSION E52167.1 GI:18629630
KEYWORDS JP 2001029077-A/3.
SOURCE unclassified

ORGANISM

unidentified

unclassified.

REFERENCE
1 (bases 1 to 769)
AUTHORS
Koyanagi, M., Koseki, Y. and Kodai, T.
TITLE
Novel MITE-like factor
JOURNAL
Patent: JP 2001029077-A 3 06-FEB-2001;

COMMENT

YOSHIHIRO KOSEKI, SAN EI GEN FFI INC
OS
Daucus carota L. cv. Kurodagosun (Carrot)
PN
JP 2001029077-A/3
PD
06-FEB-2001
PF
21-JUL-1999 JP 1999206316

PR

PI
MIXIKO KOYANAGI, YOSHIHIRO KOSEKI, TAKAOSHI KODA PC
C12N15/09//A01H1/00, C12N5/10, (C12N15/09, C12R1:91), C12N15/00, PC
C12N5/00,
PC
(C12N15/00, C12R1:91)

CC

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FT

FEATURES

source

source

source

source

source

source

source

source

source

source

source

source

source

source

source

source

source

source

source

source

source

source

source

source

source

source

source

source

source

source

source

source

source

source

source

source

source

source

source

source

source

source

source

source

source

source

source

Search completed: July 4, 2004, 23:13:24
Job time : 3465 secs

Query Match	100.0%;	Score 769;	DB 4;	Length 769;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 769;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

[illegible]

PV	MO200105986-A2.
PD	25-JAN-2001.
PP	19-JUL-2000; 2000MCO-JP004837.
PR	21-JUL-1999; 99JP-00206316.
PR	21-JUL-1999; 99JP-00206320.
PR	12-JUN-2000; 2000JP-00175825.
PA	(SANE-) SAN-EI GEN FFI INC.
PA	(OZEK/) OZEKI Y.
PI	Ozeki Y., Oyaneagi M., Fukuda T., Koda T,
DR	WPI; 2001-147351/15.
XX	
PT	Novel miniature inverted-repeat transposable element (MITE)-like element useful for constructing transgene expression cassette for stably creating genetically engineered organisms capable of expression of transgene.
PS	Claim 4; Page 99-100; 104pp; English.
CC	The present invention relates to a miniature inverted-repeat transposable element (MIRE)-like element capable of causing duplication of a target sequence at the site of its insertion in a genomic gene. The invention is useful for causing expression of a transgene in a plant. It can also be used for inducing or regulating the expression in a plant of the gene introduced
CC	
XX	
SQ	Sequence 1192 BP; 410 A; 214 C; 192 G; 376 T; 0 U; 0 Other;
	Query Match 100.0%; Score 769; DB 4; Length 1192;
	Best Local Similarity 100.0%; Pred. No. 0;
	Matches 769; Conservative 0; Mismatches 0; Indels 0; Gaps 0
CY	1 GGGATCTTTTAAAAAATTCACATCTGTAAATTATTTTTTAAAAAATCTACACTTTT 60
DB	399 GGGATCTTTTAAAAAATTCACATCTGTAAATTATTTTTTAAAAAATCTACACTTTT 458
CY	61 TCATGTTTTTAAAAAATACCTTTTCATAAATTTTTTTTTCAAAAATAGATTGCCACT 120
DB	459 TCATGTTTTTAAAAAATACCTTTTCATAAATTTTTTTTTCAAAAATAGATTGCCACT 518
CY	121 TTTCGAACCTCATTTTGCAACCTTGGCGCGCAGCCGTAAGAAGTGCAGTAGAGTTGCA 180
DB	519 TTTCGAACCTCATTTTGCAACCTTGGCGCGCAGCCGTAAGAAGTGCAGTAGAGTTGCA 578
CY	181 AAAGTTGCAAAATGAGTTGTAAAAAGTTGCAAAATGAGTTGCAAAAGTTGCAAAAT 240
DB	579 AAAGTTGCAAAATGAGTTGTAAAAAGTTGCAAAATGAGTTGCAAAAGTTGCAAAAT 638
CY	241 GGAAAGTTGCAAAAGTTGCAAACTGTGAATGCAATGATGCAAACTGAATGATGATG 300
DB	639 GGAAAGTTGCAAAAGTTGCAAACTGTGAATGCAATGATGCAAACTGAATGATGATG 698
CY	301 AAAAGTTGCAAAATGAGTTGCAAACTGAATGCAAACTGAATGCAAACTGAATGCA 360
DB	699 AAAAGTTGCAAAATGAGTTGCAAACTGAATGCAAACTGAATGCAAACTGAATGCA 758
CY	361 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
DB	759 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 818
CY	421 CAACGTGAATACAATATGCAATCATATATGCAATTAACAAATCTGATTTCAAGTTGCA 480
DB	819 CAACGTGAATACAATATGCAATCATATATGCAATTAACAAATCTGATTTCAAGTTGCA 878
CY	481 GTTTTGGATATGATTTTGGAAATGCAATATATATATATATATATATATATGATTTGCA 540
DB	879 GTTTTGGATATGATTTTGGAAATGCAATATATATATATATATATATATATGATTTGCA 938
CY	541 AATGATATGCAAAATGGAATCTGAAATCGAATTAAGGATGCAATATGATGATGCAAAA 600

Db 939 AATGACATTCGAAAACCTGAACTTGAATCAGGAATTCAGCTGATATGAAGTTGCAAAA 998
Qy 601 GAGTTTGCAACACGCGCTGGCGCCGCTGAGTTGCAAAATGAGAGTTGCAAAAAGTTGCAAC 660
Db 999 GAGGTTGCAACACGCGCTGGCGCCGCTGAGTTGCAAAATGAGAGTTGCAAAAAGTTGCAAC 1056
Qy 661 AGTATTTTGGAAAAAGATTTTATGAAAAGGATTTTAAATAATATTTCTGGAAGTTAG 720
Db 1059 AGTATTTTGGAAAAAGATTTTATGAAAAGGATTTTAAATAATATTTCTGGAAGTTAG 1118
Qy 721 TATTTTGAACAATTAATAAGAAAGTAGTATTTTGTAGATTTCC 769
Db 1119 TATTTTGAACAATTAATAAGAAAGTAGTATTTTGTAGATTTCC 1167

RESULT 3
ID AAF56298 standard; DNA; 1543 BP.
XX AAF56298;
AC AAF56298;
XX
XX 18-APR-2001 (first entry)
XX
XX IS2 element sequence #5.
XX
XX Miniature inverted repeat transposable element; MITE; duplication;
XX regulate; IS2; ds.
XX
XX Daucus carota.
XX
XX WO200105986-A2.
XX
XX 25-JAN-2001.
XX
XX 19-JUL-2000; 2000WO-JP004837.
XX
XX 21-JUL-1999; 99JP-00206316.
XX 21-JUL-1999; 99JP-00206320.
XX 12-JUN-2000; 2000JP-00175825.
XX
XX (SAME-) SAN-EI GEN FFI INC.
XX (OZEK/) OZEK/ Y.
XX
XX Ozeki Y, Oyanagi M, Fukuda T, Koda T;
XX
XX WPI; 2001-147351/15.
XX
XX Novel miniature inverted-repeat transposable element (MITE)-like element
XX useful for constructing transgene expression cassette for stably creating
XX genetically engineered organisms capable of expression of transgene.
XX
XX Disclosure: Page 103-104; 104pp; English.
XX
XX The present invention relates to a miniature inverted-repeat transposable
XX element (MITE)-like element capable of causing duplication of a target
XX sequence at the site of its insertion in a genomic gene. The invention is
XX useful for causing expression of a transgene in a plant. It can also be
XX used for inducing or regulating the expression in a plant of the gene
XX introduced
XX
XX Sequence 1543 BP; 569 A; 244 C; 214 G; 516 T; 0 U; 0 Other;
SQ

Query Match 100.0%; Score 769; DB 4; Length 1543;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 769; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGATCTTTTAAATAATCCATCTGTAAATTTTATTTTAAATAATCTACATCTTTT 60
Db 756 GGGATCTTTTAAATAATCCATCTGTAAATTTTATTTTAAATAATCTACATCTTTT 815
Qy 61 TCAATGTTTTTAAATAATCTTTTCAATAATTTTATTTTCAAAAATGCAATTTGCAACT 120

Db 816 TCAATGTTTTTAAATAATCTTTTCAATAATTTTATTTTCAAAAATGCAATTTGCAACT 875
Qy 121 TTTCGAACCTTCATTTGCAACCTTGGGCGGCGCACCCGTAAAGTTGCGAGTTGCA 180
Db 876 TTTCGAACCTTCATTTGCAACCTTGGGCGGCGCACCCGTAAAGTTGCGAGTTGCA 935
Qy 181 AAAGTTGCAAAATGAGTTTGTAAAGTTGCAAAATGAGTTGCAAAAGTTGCAAAAT 240
Db 936 AAAGTTGCAAAATGAGTTTGTAAAGTTGCAAAATGAGTTGCAAAAGTTGCAAAAT 995
Qy 241 GGAAGTTGCAACAGTTGCAACCTGCAATGCAATGCAATGCAATGCAATGCAATGCA 300
Db 996 GGAAGTTGCAACAGTTGCAACCTGCAATGCAATGCAATGCAATGCAATGCAATGCA 1055
Qy 301 AAAGTTGCAAAATGAGTTGCAACCTGCAATGCAATGCAATGCAATGCAATGCAATG 360
Db 1056 AAAGTTGCAAAATGAGTTGCAACCTGCAATGCAATGCAATGCAATGCAATGCAATG 1115
Qy 361 ATGGTGTGCCCCCTGGCGGCGCCGCTGAGTTTACATAGATGCAATGCAATGCAATG 420
Db 1116 ATGGTGTGCCCCCTGGCGGCGCCGCTGAGTTTACATAGATGCAATGCAATGCAATG 1175
Qy 421 CAACTGAATGCAACCTATATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCA 480
Db 1176 CAACTGAATGCAACCTATATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCA 1235
Qy 481 GTTTTGAATGCTATTTTGGAAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 540
Db 1236 GTTTTGAATGCTATTTTGGAAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 1295
Qy 541 AATGACATTCGAAAACTGGAACCTTGAATCAGGAATCAGCTGCAATGGAAGTTGCAAAA 600
Db 1296 AATGACATTCGAAAACTGGAACCTTGAATCAGGAATCAGCTGCAATGGAAGTTGCAAAA 1355
Qy 601 GAGGTTGCAACACGCGCTGGCGCCGCTGTAGTTGCAAAATGAGTTGCAAAAAGTTGCAAC 660
Db 1356 GAGGTTGCAACACGCGCTGGCGCCGCTGTAGTTGCAAAATGAGTTGCAAAAAGTTGCAAC 1415
Qy 661 AGTATTTTGGAAAAAGATTTTATGAAAAGGATTTTAAATAATATTTCTGGAAGTTAG 720
Db 1416 AGTATTTTGGAAAAAGATTTTATGAAAAGGATTTTAAATAATATTTCTGGAAGTTAG 1475
Qy 721 TATTTTGAACAATTAATAAGAAAGTAGTATTTTGTAGATTTCC 769
Db 1476 TATTTTGAACAATTAATAAGAAAGTAGTATTTTGTAGATTTCC 1524

RESULT 4
ID AAF56295 standard; DNA; 158 BP.
XX AAF56295;
AC AAF56295;
XX
XX 18-APR-2001 (first entry)
XX
XX IS2 element sequence #2.
XX
XX Miniature inverted repeat transposable element; MITE; duplication;
XX regulate; IS2; ds.
XX
XX Daucus carota.
XX
XX WO200105986-A2.
XX
XX 25-JAN-2001.
XX
XX 19-JUL-2000; 2000WO-JP004837.
XX
XX 21-JUL-1999; 99JP-00206316.
XX 21-JUL-1999; 99JP-00206320.
XX 12-JUN-2000; 2000JP-00175825.
XX
XX (SAME-) SAN-EI GEN FFI INC.
XX

PA (OZEK/) OZEKI Y.
XX
PI Ozeki Y, Oyanagi M, Fukuda T, Koda T;
XX
DR MPI, 2001-147351/15.
XX
XX Novel miniature inverted-repeat transposable element (MITE)-like element
PT useful for constructing transgene expression cassette for stably creating
PT genetically engineered organisms capable of expression of transgene.
XX
PS Disclosure; Page 103; 104pp; English.
XX
CC The present invention relates to a miniature inverted-repeat transposable
CC element (MITE)-like element capable of causing duplication of a target
CC sequence at the site of its insertion in a genomic gene. The invention is
CC useful for causing expression of a transgene in a plant. It can also be
CC used for inducing or regulating the expression in a plant of the gene
CC introduced.
XX
SQ Sequence 158 BP; 58 A; 16 C; 35 G; 49 T; 0 U; 0 Other;
Query Match 20.5%; Score 158; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 7.2e-61;
Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 612 ACGGCTGCGCGCGCGCTGAGTTCGCAATGAGTTCGCAAAAGTTCGCAACACTATTTTGA 671
DB 1 ACGGCTGCGCGCGCGCTGAGTTCGCAATGAGTTCGCAAAAGTTCGCAACACTATTTTGA 60
QY 672 AAAAAAGATTTTATGAAAGGATATTTTAAAAATATTCGAAAGGTATGATTTTGA 731
DB 61 AAAAAAGATTTTATGAAAGGATATTTTAAAAATATTCGAAAGGTATGATTTTGA 120
QY 732 ACATTAAGAAAGGATGAGTTCGATTTTGTAGATTTCC 769
DB 121 ACATTAAGAAAGGATGAGTTCGATTTTGTAGATTTCC 158
RESULT 5
ID AAF56294 standard; DNA; 158 BP.
XX
AC AAF56294;
XX
DT 18-APR-2001 (first entry)
XX
DE IS2 element sequence #1.
XX
KM Miniature inverted repeat transposable element; MITE; duplication;
KM regulate; IS2; ds.
XX
OS Daucus carota.
XX
PN WO200105986-A2.
XX
PD 25-JAN-2001.
XX
PF 19-JUL-2000; 2000WO-JP004837.
XX
PR 21-JUL-1999; 99JP-00206316.
XX
PR 21-JUL-1999; 99JP-00206320.
XX
PR 12-JUN-2000; 2000JP-00175825.
XX
PA (SAME-) SAN-EI GEN FFI INC.
PA (OZEK/) OZEKI Y.
XX
PI Ozeki Y, Oyanagi M, Fukuda T, Koda T;
XX
DR MPI, 2001-147351/15.
XX
XX Novel miniature inverted-repeat transposable element (MITE)-like element
PT useful for constructing transgene expression cassette for stably creating
PT genetically engineered organisms capable of expression of transgene.

XX
PS Disclosure; Page 102; 104pp; English.
XX
CC The present invention relates to a miniature inverted-repeat transposable
CC element (MITE)-like element capable of causing duplication of a target
CC sequence at the site of its insertion in a genomic gene. The invention is
CC useful for causing expression of a transgene in a plant. It can also be
CC used for inducing or regulating the expression in a plant of the gene
CC introduced.
XX
SQ Sequence 158 BP; 47 A; 29 C; 17 G; 65 T; 0 U; 0 Other;
Query Match 20.5%; Score 158; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 7.2e-61;
Matches 158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGAATCTTTTAAATAATCCCATCTGTAATATTTTAAATAATGATGACATCTTT 60
DB 1 GGAATCTTTTAAATAATCCCATCTGTAATATTTTAAATAATGATGACATCTTT 60
QY 61 TCAATGTTTTTAAATAATCCATTTTCAATAATTTTTCATAAATGATGACATCTTT 120
DB 61 TCAATGTTTTTAAATAATCCATTTTCAATAATTTTTCATAAATGATGACATCTTT 120
QY 121 TTGCAACCTCATTTGCAACCTTGCGCGCGCGCGCT 158
DB 121 TTGCAACCTCATTTGCAACCTTGCGCGCGCGCGCT 158
RESULT 6
ID AAF56291/c standard; DNA; 769 BP.
XX
AC AAF56291;
XX
DT 18-APR-2001 (first entry)
XX
DE MITE-like element 5' terminal inverted repeat sequence.
XX
KM Miniature inverted repeat transposable element; MITE; duplication;
KM regulate; ds.
XX
OS Daucus carota.
XX
PN WO200105986-A2.
XX
PD 25-JAN-2001.
XX
PF 19-JUL-2000; 2000WO-JP004837.
XX
PR 21-JUL-1999; 99JP-00206316.
XX
PR 21-JUL-1999; 99JP-00206320.
XX
PR 12-JUN-2000; 2000JP-00175825.
XX
PA (SAME-) SAN-EI GEN FFI INC.
PA (OZEK/) OZEKI Y.
XX
PI Ozeki Y, Oyanagi M, Fukuda T, Koda T;
XX
DR MPI, 2001-147351/15.
XX
XX Novel miniature inverted-repeat transposable element (MITE)-like element
PT useful for constructing transgene expression cassette for stably creating
PT genetically engineered organisms capable of expression of transgene.
XX
PS Claim 4; Page 98-99; 104pp; English.
XX
CC The present invention relates to a miniature inverted-repeat transposable
CC element (MITE)-like element capable of causing duplication of a target
CC sequence at the site of its insertion in a genomic gene. The invention is
CC useful for causing expression of a transgene in a plant. It can also be
CC used for inducing or regulating the expression in a plant of the gene
CC introduced.

XX Sequence 769 BP; 277 A; 113 C; 141 G; 238 T; 0 U; 0 Other;

Query Match 14.6%; Score 112; DB 4; Length 769;
Best Local Similarity 100.0%; Pred. No. 3e-40;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 463 TCCGATTTCAAGTTCAGTTTCGATGTCATTTTCGAAATGCAATATATATATATAT 522
DB 574 TCCGATTTCAAGTTCAGTTTCGATGTCATTTTCGAAATGCAATATATATATATAT 515
QY 523 ATATATATGATTTTCGAAATGCAATTCGAAACTGGAATTCGAAATCAGGA 574
DB 514 ATATATATGATTTTCGAAATGCAATTCGAAACTGGAATTCGAAATCAGGA 463

RESULT 7
AAFS6293/c
ID AAFS6293 standard; DNA; 1192 BP.

XX AAFS6293;
AC AAFS6293;
XX 18-APR-2001 (first entry)

DE MITE-like element.

XX Miniature inverted repeat transposable element; MITE; duplication;
KM regulator; ds.

OS Dancus carota.

XX WO200105986-A2.

PD 25-JAN-2001.

PF 19-JUL-2000; 2000MO-JP004837.

XX 21-JUL-1999; 99UP-00206316.

PR 21-JUL-1999; 99UP-00206320.

PR 12-JUN-2000; 2000JP-00175825.

XX (SANE-) SAN-EI GEN FFI INC.

PA (OZEK/) OZEKI Y.

PI Ozeki Y, Oyanagi M, Fukuda T, Koda T;

XX WPI; 2001-147351/15.

PT Novel miniature inverted-repeat transposable element (MITE)-like element
PT useful for constructing transgene expression cassette for stably creating
PT genetically engineered organisms capable of expression of transgene.

PS Claim 4; Page 99-100; 104pp; English.

XX The present invention relates to a miniature inverted-repeat transposable
CC element (MITE)-like element capable of causing duplication of a target
CC sequence at the site of its insertion in a genomic gene. The invention is
CC useful for causing expression of a transgene in a plant. It can also be
CC used for inducing or regulating the expression in a plant of the gene
CC introduced

CC Sequence 1192 BP; 410 A; 214 C; 192 G; 376 T; 0 U; 0 Other;

SO Query Match 14.6%; Score 112; DB 4; Length 1192;
Best Local Similarity 100.0%; Pred. No. 3e-40; Indels 0; Gaps 0;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 463 TCCGATTTCAAGTTCAGTTTCGATGTCATTTTCGAAATGCAATATATATATATAT 522
DB 972 TCCGATTTCAAGTTCAGTTTCGATGTCATTTTCGAAATGCAATATATATATATAT 913
QY 523 ATATATATGATTTTCGAAATGCAATTCGAAACTGGAATTCGAAATCAGGA 574

DB 912 ATATATATGATTTTCGAAATGCAATTCGAAACTGGAATTCGAAATCAGGA 861

RESULT 8
AAFS6298/c
ID AAFS6298 standard; DNA; 1543 BP.

XX AAFS6298;

AC AAFS6298;
XX 18-APR-2001 (first entry)

DE IS2 element sequence #5.

XX Miniature inverted repeat transposable element; MITE; duplication;
KM regulator; IS2; ds.

OS Dancus carota.

XX WO200105986-A2.

PD 25-JAN-2001.

PF 19-JUL-2000; 2000MO-JP004837.

XX 21-JUL-1999; 99UP-00206316.

PR 21-JUL-1999; 99UP-00206320.

PR 12-JUN-2000; 2000JP-00175825.

XX (SANE-) SAN-EI GEN FFI INC.

PA (OZEK/) OZEKI Y.

PI Ozeki Y, Oyanagi M, Fukuda T, Koda T;

XX WPI; 2001-147351/15.

PT Novel miniature inverted-repeat transposable element (MITE)-like element
PT useful for constructing transgene expression cassette for stably creating
PT genetically engineered organisms capable of expression of transgene.

PS Disclosure; Page 103-104; 104pp; English.

XX The present invention relates to a miniature inverted-repeat transposable
CC element (MITE)-like element capable of causing duplication of a target
CC sequence at the site of its insertion in a genomic gene. The invention is
CC useful for causing expression of a transgene in a plant. It can also be
CC used for inducing or regulating the expression in a plant of the gene
CC introduced

CC Sequence 1543 BP; 569 A; 244 C; 214 G; 516 T; 0 U; 0 Other;

SO Query Match 14.6%; Score 112; DB 4; Length 1543;
Best Local Similarity 100.0%; Pred. No. 3e-40; Indels 0; Gaps 0;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 463 TCCGATTTCAAGTTCAGTTTCGATGTCATTTTCGAAATGCAATATATATATATAT 522
DB 1332 TCCGATTTCAAGTTCAGTTTCGATGTCATTTTCGAAATGCAATATATATATATAT 1270
QY 523 ATATATATGATTTTCGAAATGCAATTCGAAACTGGAATTCGAAATCAGGA 574
DB 1269 ATATATATGATTTTCGAAATGCAATTCGAAACTGGAATTCGAAATCAGGA 1218

RESULT 9
AAFS6294/c
ID AAFS6294 standard; DNA; 158 BP.

XX AAFS6294;

AC AAFS6294;
XX 18-APR-2001 (first entry)

DE IS2 element sequence #1.

XX

KW Miniature inverted repeat transposable element; MITE; duplication;
KM regulate; IS2; ds.
XX
XX Daucus carota.
OS
XX WO200105986-A2.
PN
XX
XX 25-JAN-2001.
PD
XX
XX 19-JUL-2000; 2000WO-JP004837.
PF
XX
XX 21-JUL-1999; 99JP-00206316.
PR
XX 21-JUL-1999; 99JP-00206320.
PR
XX 12-JUN-2000; 2000JP-00175825.
XX
XX (SANE-) SAN-EI GEN FFI INC.
PA
XX (OZEK/) OZEKI Y.
PI
XX Ozeki Y, Oyanagi M, Fukuda T, Koda T;
PI
XX WPI; 2001-147351/15.
DR
XX
XX Novel miniature inverted-repeat transposable element (MITE)-like element
PT useful for constructing transgene expression cassette for stably creating
PT genetically engineered organisms capable of expression of transgene.
XX
XX Disclosure; Page 102; 104pp; English.
PS
XX
XX The present invention relates to a miniature inverted-repeat transposable
CC element (MITE)-like element capable of causing duplication of a target
CC sequence at the site of its insertion in a genomic gene. The invention is
CC useful for causing expression of a transgene in a plant. It can also be
CC used for inducing or regulating the expression in a plant of the gene
CC introduced
CC
XX
SQ Sequence 158 BP; 47 A; 29 C; 17 G; 65 T; 0 U; 0 Other;
Query Match 3.9%; Score 30; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 205 GTTGC AATGAGGTGCAAAAGTTGCAAT 234
DB 140 GTTGC AATGAGGTGCAAAAGTTGCAAT 111
RESULT 10
AAF56295/C
ID AAF56295 standard; DNA; 158 BP.
XX
XX AAF56295;
AC
XX 18-APR-2001 (first entry)
DT
XX
XX IS2 element sequence #2.
DE
XX
XX Miniature inverted repeat transposable element; MITE; duplication;
KM regulate; IS2; ds.
XX
XX Daucus carota.
OS
XX
XX WO200105986-A2.
PN
XX
XX 25-JAN-2001.
PD
XX
XX 19-JUL-2000; 2000WO-JP004837.
PF
XX
XX 21-JUL-1999; 99JP-00206316.
PR
XX 21-JUL-1999; 99JP-00206320.
PR
XX 12-JUN-2000; 2000JP-00175825.
XX
XX (SANE-) SAN-EI GEN FFI INC.
PA
XX (OZEK/) OZEKI Y.

XX Ozeki Y, Oyanagi M, Fukuda T, Koda T;
PI
XX WPI; 2001-147351/15.
DR
XX
XX Novel miniature inverted-repeat transposable element (MITE)-like element
PT useful for constructing transgene expression cassette for stably creating
PT genetically engineered organisms capable of expression of transgene.
XX
XX Disclosure; Page 103; 104pp; English.
PS
XX
XX The present invention relates to a miniature inverted-repeat transposable
CC element (MITE)-like element capable of causing duplication of a target
CC sequence at the site of its insertion in a genomic gene. The invention is
CC useful for causing expression of a transgene in a plant. It can also be
CC used for inducing or regulating the expression in a plant of the gene
CC introduced
CC
XX
SQ Sequence 158 BP; 58 A; 16 C; 35 G; 49 T; 0 U; 0 Other;
Query Match 3.8%; Score 29; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.0052;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 112 TTTCGCACTTTGCAACCTCATTTGCAAC 140
DB 48 TTTCGCACTTTGCAACCTCATTTGCAAC 20
RESULT 11
AB21958
ID AB21958 standard; DNA; 2717 BP.
XX
XX AB21958;
AC
XX 26-MAR-2002 (first entry)
DT
XX
XX Drosophila melanogaster genomic polynucleotide SEQ ID NO 17347.
DE
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
KM pharmaceutical; gene; ds.
XX
XX Drosophila melanogaster.
OS
XX
XX WO200171042-A2.
PN
XX
XX 27-SEP-2001.
PD
XX
XX 23-MAR-2001; 2001WO-US009231.
PF
XX
XX 23-MAR-2000; 2000US-0191637P.
PR
XX 11-JUL-2000; 2000US-00614150.
PR
XX
XX (PEKE) PS CORP NY.
PA
XX
XX Venter JC, Adams M, Li PWD, Myers EM;
PI
XX
XX WPI; 2001-655860/75.
DR
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions.
PT
XX
XX Claim 1; SEQ ID NO 17347; 21pp + Sequence Listing; English.
PS
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB21958-AB230511), expressed DNA
CC sequences (AB21958-AB21975) and the encoded proteins (AB219737-
CC AB219772). The sequence data for this patent did not form part of the

CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 2717 BP, 835 A; 555 C; 503 G; 824 T; 0 U; 0 Other;
Query Match 3.8%; Score 29; DB 4; Length 2717;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 501 AATCGATATATATATATATATATATATATA 529
DB 767 AATCGATATATATATATATATATATATATA 795

RESULT 12
ABL21958/C
ID ABL21958 standard; DNA; 2717 BP.
XX
AC ABL21958;
XX
DT 26-MAR-2002 (first entry)
XX
DZ Drosophila melanogaster genomic polynucleotide SEQ ID NO 17347.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ds.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li FWD, Myers EW;
XX
DR WPI; 2001-656860/75.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
PS Claim 1; SEQ ID NO 17347; 21bp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signaling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABU16176-ABU30511), expressed DNA
CC sequences (ABU1840-ABU16175) and the encoded proteins (ABBS7737-
CC ABBS7072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 2717 BP, 835 A; 555 C; 503 G; 824 T; 0 U; 0 Other;
Query Match 3.8%; Score 29; DB 4; Length 2717;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 508 TATATATATATATATATATATATATCGATT 536
DB 795 TATATATATATATATATATATATATCGATT 767

RESULT 13

ABN81058
ID ABN81058 standard; DNA; 466 BP.
XX
AC ABN81058;
XX
DT 16-JUL-2002 (first entry)
XX
DE Shrimp polynucleotide SEQ ID NO 62.
XX
KW Giant black tiger prawn; Penaeus monodon; pacific white shrimp;
KW Litopenaeus vannamei; shrimp; microsatellite sequence; genome mapping;
KW Taura Syndrome Virus; TSV; infection; ds.
XX
OS Penaeus monodon.
XX
PN WO200034476-A2.
XX
PD 15-JUN-2000.
XX
PF 10-DEC-1999; 99WO-US029571.
XX
PR 10-DEC-1998; 98US-0111670P.
XX
PA (TUFT) TUFTS COLABSE.
XX
PI Alciivar-Warren A, Xu Z, Dhar AK, Fan Y, Meenan D, Garcia DK;
XX
DR WPI; 2000-423422/36.
XX
PT Polynucleotides of shrimp are useful for identifying, mapping and
PT characterizing of the genome of various species of shrimp.
XX
PS Claim 1; Page 91; 120pp; English.
XX
CC The invention relates to an isolated polynucleotide (I) of the giant
CC black tiger prawn, Penaeus monodon or expressed sequence tags of the
CC pacific white shrimp, Litopenaeus vannamei (ABN80997-ABN81172), both
CC containing microsatellites sequences including those P. monodon
CC microsatellite sequences given in GenBank AF077550-AF077558. (I), the
CC complementary sequence or fragment and the encoded polypeptide are useful
CC for mapping of the genome of various species of shrimp. Mapping the
CC genome of Penaeus is useful for determining whether a test shrimp,
CC preferably Litopenaeus vannamei, has a genotype associated with a
CC phenotypic trait such as resistance to Taura Syndrome Virus (TSV)
CC infection
XX
SQ Sequence 466 BP, 146 A; 97 C; 91 G; 132 T; 0 U; 0 Other;
Query Match 3.6%; Score 28; DB 3; Length 466;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 503 ATCGATATATATATATATATATATATATAT 530
DB 95 ATCGATATATATATATATATATATATATATAT 122

RESULT 14
ABN81058/C
ID ABN81058 standard; DNA; 466 BP.
XX
AC ABN81058;
XX
DT 16-JUL-2002 (first entry)
XX
DE Shrimp polynucleotide SEQ ID NO 62.
XX
KW Giant black tiger prawn; Penaeus monodon; pacific white shrimp;
KW Litopenaeus vannamei; shrimp; microsatellite sequence; genome mapping;
KW Taura Syndrome Virus; TSV; infection; ds.
XX
OS Penaeus monodon.
XX

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using SW model

Run on: July 4, 2004, 22:15:37 ; Search time 2676 Seconds

(without alignments)
8561.471 Million cell updates/sec

Title: US-10-031-818b-1

Sequence score: 769
1 gggatcttcttaataacc.....ggatcttctgtagattcc 769

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Labeling first 45 summaries

Database :

EST:
1: em_escba:*
2: em_escba:*
3: em_escba:*
4: em_escba:*
5: em_escba:*
6: em_escba:*
7: em_escba:*
8: em_escba:*
9: gb_esc1:*
10: gb_esc1:*
11: gb_esc1:*
12: gb_esc1:*
13: gb_esc1:*
14: gb_esc1:*
15: em_escba:*
16: em_escba:*
17: em_escba:*
18: em_escba:*
19: em_escba:*
20: em_escba:*
21: em_escba:*
22: em_escba:*
23: em_escba:*
24: em_escba:*
25: em_escba:*
26: em_escba:*
27: em_escba:*
28: gb_esc1:*
29: gb_esc1:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	ID	Description
1	30	3.9	186	12	BI795040	BI795040 H006F09 E
2	30	3.9	186	12	BI795040	BI795040 H006F09 E
3	30	3.9	297	12	BI799513	BI799513 H134C11 E
4	30	3.9	297	12	BI799513	BI799513 H134C11 E

5	30	3.9	345	14	CB966625	CB966625 NL40_C10
6	30	3.9	345	14	CB966625	CB966625 NL40_C10
7	30	3.9	348	13	BU673472	BU673472 NL_15_82
8	30	3.9	348	13	BU673472	BU673472 NL_15_82
9	30	3.9	358	12	BI306298	BI306298 NL_4_B15
10	30	3.9	358	12	BI306298	BI306298 NL_4_B15
11	30	3.9	535	12	BI305924	BI305924 NL_2_H20
12	30	3.9	535	12	BI305924	BI305924 NL_2_H20
13	30	3.9	577	13	BU673763	BU673763 NL_19_92
14	30	3.9	577	13	BU673763	BU673763 NL_19_92
15	30	3.9	633	12	BI306166	BI306166 NL_3_007
16	30	3.9	633	12	BI306166	BI306166 NL_3_007
17	30	3.9	638	14	CB964597	CB964597 NL8_G07 D
18	30	3.9	638	14	CB964597	CB964597 NL8_G07 D
19	30	3.9	644	14	CB966543	CB966543 NL3_B06
20	30	3.9	644	14	CB966543	CB966543 NL3_B06
21	30	3.9	648	14	CB617907	CB617907 OSITEA01G
22	30	3.9	648	14	CB617907	CB617907 OSITEA01G
23	30	3.9	772	14	CB625169	CB625169 OSITEA14C
24	30	3.9	772	14	CB625169	CB625169 OSITEA14C
25	29	3.8	319	28	BH184153	BH184153 024_L_22-
26	29	3.8	319	28	BH184153	BH184153 024_L_22-
27	29	3.8	319	29	CNS07P55	AL621106 T3 end of
28	29	3.8	319	29	CNS07P55	AL621106 T3 end of
29	29	3.8	473	28	BH200037	BH200037 Sm1_53A2.
30	29	3.8	473	28	BH200037	BH200037 Sm1_53A2.
31	29	3.8	482	28	AQ970964	AQ970964 RPT-23-3
32	29	3.8	482	28	AQ970964	AQ970964 RPT-23-3
33	29	3.8	497	28	BH200889	BH200889 Sm1_41113
34	29	3.8	497	28	BH200889	BH200889 Sm1_41113
35	29	3.8	586	14	CD082704	CD082704 MA3_9939U
36	29	3.8	586	14	CD082704	CD082704 MA3_9939U
37	29	3.8	607	28	BH543165	BH543165 BOGME35TR
38	29	3.8	607	28	BH543165	BH543165 BOGME35TR
39	29	3.8	733	29	BX235983	BX235983 Danilo rer
40	29	3.8	733	29	BX235983	BX235983 Danilo rer
41	28	3.6	210	29	CG314411	CG314411 OGB0Q35TH
42	28	3.6	210	29	CG314411	CG314411 OGB0Q35TH
43	28	3.6	330	28	B2198852	B2198852 CH230-494
44	28	3.6	330	28	B2198852	B2198852 CH230-494
45	28	3.6	333	12	BI504445	BI504445 BB170002A

ALIGNMENTS

RESULT 1
BI795040
LOCUS
DEFINITION
H006F09 Endospore library from *Oryza sativa* (10 days after
anthesis) *Oryza sativa* cDNA clone H006F09, mRNA sequence.

ACCESSION
BI795040.1 GI:15846764

VERSION
KEYWORDS
SOURCE

ORGANISM
Oryza sativa

REFERENCE
AUTHORS

TITLE
JOURNAL

COMMENT

CONTACT: Haitao Dong, Debao Li

Bioinformatics and Gene Network Research Group

Zhejiang University

Kaixuan Road, 268#, Hangzhou, Zhejiang, P.R.China

Tel: 0086-571-86892051

Fax: 0086-571-86961525

Email: webmaster@estarray.org, URL: http://www.estarray.org

Seq primer: M13 forward primer.

Location/Qualifiers


```

/mol_type="tRNA"
/db_xref="taxon:4530"
/clone="H134C11"
/tissue_type="Endosperm"
/development="10 days after anthesis"
/clone_library="Endosperm library from Oryza sativa (10 days after anthesis)"
/note="Vector: pSport2"

```

		Query Match	3.9%;	Score 30;	DB 12;	Length 297;
		Best Local Similarity	100.0%;	Pred. No. 0.13;		
		Matches	30;	Conservative	0;	Mismatches
					0;	Indels
					0;	Gaps
Qy	501	AAATCGATAATATATATATATATATAT	530			
Dd	177	AAATCGATAATATATATATATATATAT	148			

RESULT 5	CB966625	LOCUS	DEFINITION	ACCESSION:	VERSION	KEYWORDS	SOURCE	ORGANISM
	CB966625	345 bp	mRNA	linear	EST 29-APR-2001			
	MDA_C10	Drought stress (leaf)	Oryza sativa (indica cultivar-group)	CDNA clone MDA_C10 3', mRNA sequence.				
	CB966625							
	CB966625.1	GI:30228735	EST.					
	Oryza sativa (indica cultivar-group)							
	Oryza sativa (indica cultivar-group)							

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (Pages 1 to 345)	Markandeya, G., Ravindra Babu, P., Venkat Reddy, B., Nagabushana, I., Chandra Sekhar, A., Bonnerzen, J. L., Ramakrishna, W. and Reddy, A.R.	ESTs from a normalized cDNA library of drought stressed rice seedlings (Oryza sativa L. cv Nagina 22)	Unpublished (2003)	Contact: Reddy AR

Department of Plant Sciences
University of Hyderabad
P.O. Central University, Hyderabad-500 046, A.P., India
Tel.: 0091-40-3010265
Fax: 0091-40-3010145
Email: arjun@uhyd.ernet.in
Insert Length: 345 Std Error: 0.00
Seq primer: CCGCAGGTTTCACGTACGAC.

```

source
1. .345
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="cRNA"
/cultivar="Magina 22 (indica sub sp)"
/db_xref="taxon:39946"
/clome="NL40_C10"
/tissue_type="Entire leaf tissue"
/dev_stage="35 day-old seedlings"
/clome_1lb="Drought stress (leaf)"
/note="Organ: Leaf; Vector: T73Bac; ESTs from normalized
leaf cDNA library from drought stressed seedlings"

```

Query Match	3.9%	Score 30	DB 14	Length 345
Best Local Similarity	100.0%	Pred. No. 0.12		
Matches 30	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	501	AAATCGATATATATATATATATATAT	530	
DB	106	AAATCGATATATATATATATATATAT	135	

RESULT 6	
CB966625/c	
LOCUS	CB966625
	345 bp
	mRNA
	linear
	EST 29-APR-2001

DEFINITION	NI40 C10 Drought stress (leaf) <i>Oryza sativa</i> (indica cultivar-group) cDNA clone NI40_C10 3', mRNA sequence.
ACCESSION	CB966625
VERSION	CB966625.1 GI:30228735
KEYWORDS	EST.
SOURCE	<i>Oryza sativa</i> (indica cultivar-group)
ORGANISM	<i>Oryza sativa</i> (indica cultivar-group)
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; <i>Oryza</i> .
AUTHORS	1 (bases 1 to 345) Markandeya,G., Ravindra Babu,P., Venkat Reddy,B., Nagabushana,I., Chandra Sekhar,A., Benmetzen,J.L., Ramakrishna,M. and Reddy,A.R.
TITLE	ESTs from a normalized cDNA library of drought stressed rice seedlings (<i>Oryza sativa</i> L.cv Nagina 22)
JOURNAL	Unpublished (2003)
COMMENT	Contact: Reddy AR Department of Plant Sciences, School of Life Sciences University of Hyderabad P.O. Central University, Hyderabad-500 046, A.P., India Tel: 0091-40-3010265 Fax: 0091-40-3010145 Email: arjuls@uohyd.ernet.in Insert length: 345 Std Error: 0.00 Seq primer: GCGCAGGTTTCCACATCAGCAGC.
FEATURES	Location/Qualifiers
SOURCE	1..345

Query	March	3.9%	Score 30;	DB 14;	Length 345;
Best Local Similarity		100.0%	Pred. No. 0.12;		
Matches	30;	Conservative	0;	Mismatches	0;
				Indels	0;
				Gaps	0;
QY	507	AAATATATATATATATATATATTCAGTTT	536		
	135	AAATATATATATATATATATTCAGTTT	106		

RESULT	7
BUE673472	
LOCUS	BU673472
DEFINITION	BU673472 348 bp mRNA linear EST 07-OCT-2002 NL_15_82 Drought stress (leaf) Oryza sativa (indica cultivar-group)
ACCESSION	CN_15_g1one.NL_15_82.3 , mRNA sequence.
VERSION	BU673472
KEYWORDS	BU673472.1 GI:23514110
SOURCE	EST .
ORGANISM	Oryza sativa (indica cultivar-group) Oryza sativa (indica cultivar-group) Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Erbartoideae; Oryzaceae; Oryza. I (bases 1 to 348)
REFERENCE	Reddy,A.R., Makhandev,G., Ramakrishna,W., Nagabhushana,I., Ravindra Babu,P., Madana Mohan Reddy,A., Chandra Sekhar,A. and Bennetzen,J.L.
TITLE	Novel EST enrichment with normalized cDNA libraries from drought stressed rice (Oryza sativa L.cv Nagina 22) (2002)
JOURNAL	Unpublished (2002)
COMMENT	Contact: Reddy AR

Department of Plant Sciences, School of Life Sciences
University of Hyderabad
P.O. Central University, Hyderabad-500 046, A.P., India
Tel: 0091-40-3010265

Fax: 0091-40-3010145
Email: arjulis@uohyd.ernet.in
Insert length: 348 Std Error: 0.00
Seq primer: CGCCAGGTTTCCGACGACGAC.

FEATURES

Location/Qualifiers

SOURCE

ORIGIN

Query Match 3.9%; Score 30; DB 13; Length 348;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 501 AATCGATATATATATATATATATATAT 530
Db 109 AATCGATATATATATATATATATATAT 138

RESULT 8 BUE73472 348 bp mRNA linear EST 07-OCT-2002
LOCUS BUE73472/c NL_15_82 Drought stress (leaf) Oryza sativa (indica cultivar-group)
DEFINITION BUE73472.1 GI:23514110
ACCESSION BUE73472
VERSION BUE73472.1 GI:23514110
KEYWORDS EST.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Erbartoideae; Oryzaceae; Oryza.

REFERENCE

1 (bases 1 to 348)
Reddy,A.R., Markandeya,G., Ramakrishna,W., Nagabhushana,I.,
Ravindra Babu,P., Madana Mohan Reddy,A., Chandra Sekhar,A. and
Bennetzen,J.L.
Novel EST enrichment with normalized cDNA libraries from drought
stressed rice (Oryza sativa L.cv Nagina 22) (2002)
Unpublished (2002)
Contact: Reddy AR
Department of Plant Sciences, School of Life Sciences
University of Hyderabad
P.O. Central University, Hyderabad-500 046, A.P, India
Tel: 0091-40-3010265
Fax: 0091-40-3010145
Email: arjulis@uohyd.ernet.in
Insert length: 348 Std Error: 0.00
Seq primer: CGCCAGGTTTCCGACGACGAC.

AUTHORS

1 (bases 1 to 348)
Reddy,A.R., Markandeya,G., Ramakrishna,W., Nagabhushana,I.,
Ravindra Babu,P., Madana Mohan Reddy,A., Chandra Sekhar,A. and
Bennetzen,J.L.
Novel EST enrichment with normalized cDNA libraries from drought
stressed rice (Oryza sativa L.cv Nagina 22) (2002)
Unpublished (2002)
Contact: Reddy AR
Department of Plant Sciences, School of Life Sciences
University of Hyderabad
P.O. Central University, Hyderabad-500 046, A.P, India
Tel: 0091-40-3010265
Fax: 0091-40-3010145
Email: arjulis@uohyd.ernet.in
Insert length: 348 Std Error: 0.00
Seq primer: CGCCAGGTTTCCGACGACGAC.

JOURNAL COMMENT
Unpublished (2002)
Contact: Reddy AR
Department of Plant Sciences, School of Life Sciences
University of Hyderabad
P.O. Central University, Hyderabad-500 046, A.P, India
Tel: 0091-40-3010265
Fax: 0091-40-3010145
Email: arjulis@uohyd.ernet.in
Insert length: 348 Std Error: 0.00
Seq primer: CGCCAGGTTTCCGACGACGAC.

FEATURES

Location/Qualifiers

SOURCE

1. 348
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nagina 22 (indica sub sp)"
/db_xref="taxon:39946"
/clone="NL_15_82"
/tissue_type="Bartire leaf tissue"
/dev_stage="35 day-old seedlings"
/clone_lib="Drought stress (leaf)"
/note="Organ: Leaf; Vector: T773Pac; ESTs from normalized
leaf cDNA library from drought stressed seedlings"

ORIGIN

Query Match 3.9%; Score 30; DB 13; Length 348;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 507 ATATATATATATATATATATATATATATAT 536
Db 138 ATATATATATATATATATATATATATATAT 109

RESULT 9 BI306298 358 bp mRNA linear EST 20-JUL-2001
LOCUS BI306298 NL_4_B15 Drought stress (leaf) Oryza sativa (indica cultivar-group)
DEFINITION BI306298.1 GI:14981620
ACCESSION BI306298
VERSION BI306298
KEYWORDS EST.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Erbartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 358)
Reddy,A.R., Ramakrishna,W., Chandrasekhar,A., Nagabhushan,I.,
Ravindra Babu,P. and Bennetzen,J.L.
Novel EST enrichment with normalized cDNA libraries from drought
stressed rice (Oryza sativa L.cv Nagina 22)
Unpublished (2001)
Contact: Reddy AR
Department of Plant Sciences, School of Life Sciences
University of Hyderabad
P.O. Central University, Hyderabad-500 046, A.P, India
Tel: 0091-40-3010265
Fax: 0091-40-3010145
Email: arjulis@uohyd.ernet.in
Insert length: 358 Std Error: 0.00
Plate: 4 row: B Column: 15
Seq primer: GTAAAACGACGCGACGACG.

FEATURES

Location/Qualifiers

SOURCE

1. 358
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nagina 22 (indica sub sp)"
/db_xref="taxon:39946"
/clone="NL_4_B15"
/tissue_type="Bartire leaf tissue"
/dev_stage="35 day-old seedlings"
/clone_lib="Drought stress (leaf)"
/note="Organ: Leaf; Vector: T773Pac; ESTs from normalized
leaf cDNA library from drought stressed seedlings"

ORIGIN

Query Match 3.9%; Score 30; DB 12; Length 358;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 501 AATCGATATATATATATATATATATAT 530
Db 109 AATCGATATATATATATATATATATAT 138

RESULT 10 BI306298/c 358 bp mRNA linear EST 20-JUL-2001
LOCUS BI306298 NL_4_B15 Drought stress (leaf) Oryza sativa (indica cultivar-group)
DEFINITION BI306298.1 GI:14981620
ACCESSION BI306298
VERSION BI306298
KEYWORDS EST.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Erbartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 358)
Reddy,A.R., Ramakrishna,W., Chandrasekhar,A., Nagabhushan,I.,

TITLE Ravindrababu, P. and Bennetzen, J.L.
Novel BGT enrichment with normalised cDNA libraries from drought
stressed rice (Oryza sativa L. cv Nagina 22)
JOURNAL Unpublished (2001)
COMMENT Contact: Reddy AR

Department of Plant Sciences, School of Life Sciences
University of Hyderabad
P.O. Central University, Hyderabad-500 046, A.P., India
Tel.: 0091-40-3010265
Fax: 0091-40-3010145
Email: arjuls@uohyd.ernet.in
Insert Length: 358 Std Error: 0.00
Plate: 4 row: B column: 15
Seq primer: GTAAACCAACCGCCAGTC
Location/Qualifiers

```

/organism="Oryza sativa (indica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nagina 22 (indica sub sp)"
/cdb_xref="taxon:39346"
/clone="NI_4.B15"
/tissue_type="Entire leaf tissue"
/dev_stage="35 day-old seedlings"
/clone_1b="Drought stress (leaf)"
/notes="Organ: leaf; Vector: T7T3pac; ESTs from normalized
leaf cDNA library from drought stressed seedlings"

```

	Query Match	3.9%	Score 30;	DB 12;	Length 358;
	Best Local Similarity	100.0%	Pred. No.	0.12;	
	Matches	30;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0
Cy	ATATTATATATATATATATATGATT	536			
Db	ATATATATATATATATATATCATTTT	109			

RESULT 11					
B1305924					
LOCUS					
DEFINITION	B1305924	535 bp	mRNA	linear	EST 20-JUL-2001
	NL_2_H20 Drought stress		(leaf)	Oryza sativa	(indica cultivar-group)
	cdna_2 clone NL_2_H20_3',		mRNA sequence.		
ACCESSION	B1305924				
VERSION	B1305924.1	GI:14981246			
KEYWORDS	EST.				
SOURCE	Oryza sativa (indica cultivar-group)				

REFERENCE
1 (bases 1 to 535)
Reddy A.R., Ramakrishna, W., Chandrasekhar, A., Nagabushan, I.,
Nayindrababu, P. and Bennetzen, J.L.
TITLE
Novel EST enrichment with normalised cDNA libraries from drought
stressed rice (*Oryza sativa* L. cv Nagina 22)
JOURNAL
Unpublished (2001)
COMMENT
Contact: Reddy AR

University of Hyderabad
P.O. Central University, Hyderabad-500 046, A.P. India
Tel.: 0091-40-3010265
Fax: 0091-40-3010145
Email: arjuls@uohyd.ernet.in
Insert Length: 535 Std Error: 0.00
Plate: 2 row: H column: 20
Seq primer: GTAAACGACGGCAGCG.
Location/Qualifiers
1. 535

```

/tissue_type="Entire leaf tissue"
/dev_stage="35 day-old seedlings"
/clone_lib="Drought stress (leaf)"
/notes="Organ: leaf; Vector: TTY3pac; ESTs from normalized
leaf cDNA library from drought stressed seedlings "

```

	Query Match	3.9%	Score 30;	DB 12;	Length 535;
	Best Local Similarity	100.0%;	Pred. No.	0.095;	
	Matches	30;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	ATTATGTTATCATATGATACTTTCGGATTT	536			
Dd	ATTATGTTATGATTAATATGACGAATTT	418			

RESULT 12	BI305924/c	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
	BI305924	535 bp	mRNA	linear	EST 20-JUL-2003			
	ML_2_H20	Drought stress (leaf)	Oryza sativa	(indica cultivar-group)				
	cDNA clone ML_2_H20_3	'	mRNA sequence.					
	BI305924							
	BI305924.1	GI:14981246						
	EST.							
	Oryza sativa	(indica cultivar-group)						
	Oryza sativa	(indica cultivar-group)						

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (Pages 1 to 515)	Reddy, A.R., Ramakrishna, W., Chandrasekhar, A., Nagabhushan, I., Ravindrababu, P. and Bennetzen, J. L.	Novel EST enrichment with normalized cDNA libraries from drought stressed rice (<i>Oryza sativa</i> L. cv Nagina 22)	Unpublished (2001)	Contact: Reddy AR

Department of Plant Sciences, School of Life Sciences
University of Hyderabad
P.O. Central University, Hyderabad-500 046, A.P., India
Tel: 0091-40-3010265
Fax: 0091-40-3010145
Email: arjuls@uohyd.ernet.in
Insert Length: 535 Std Error: 0.00
Plate: 2 row: H column: 20
Seq primer: GTAAAAGACGCCCAATG.
Location/Qualifiers

```

Source
1..535
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nagina 22 (indica sub sp)"
/db_xref="caxon:39946"
/clone="NL 2 H20"
/tissue_type="Entire leaf tissue"
/dev_stage="15 day-old seedlings"
/clone_id="Drought stress (leaf)"
/note="Organ: Leaf, Vector: pTRIPac, ESTs from normalized
leaf cDNA library from drought stressed seedlings"

```

RESULT 13	LOCUS	DEFINITION
BUE73763	577 bp	mRNA
NU_19_92	Drought stress (leaf)	Oryza sativa (indica cultivar-group)
CDNA clone NU_19_92.3	mRNA sequence.	

ACCESSION	BUE73763		GI:23514684	
VERSION	BUE73763.1			
KEYWORDS	EST.			
SOURCE	Oryza sativa (indica cultivar-group)			
ORGANISM	Oryza sativa (indica cultivar-group)			
	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
	Spermatophyte; Magnoliophyta; Liliopsida; Poales; Poaceae;			
	Ehretoidae; Oryzaceae; Oryza.			
REFERENCE	1 (bases 1 to 577)			
AUTHORS	Reddy A.R., Marikandeya,G., Ramakrishna,W., Nagabushana,I., Ravindra Babu,P., Madana Mohan Reddy,A., Chandra Sekhar,A. and Benneetzen,J.L.			
TITLE	Novel EST enrichment with normalized cDNA libraries from drought stressed rice (Oryza sativa L.cv Nagina 22) (2002)			
JOURNAL	Unpublished (2002)			
COMMENT	Contact: Reddy AR Department of Plant Sciences, School of Life Sciences University of Hyderabad P.O. Central University, Hyderabad-500 046, A.P, India Tel.: 0091-40-3010265 Fax: 0091-40-3010145 Email: arjula@omhyd.ernet.in Insert Length: 577 Std Error: 0.00 Seq primer: CGCCAGGCTTCCAGGTCCAGCAGCACGAC. Location/Qualifiers 1..577 /organism="Oryza sativa (indica cultivar-group)" /mol_type="mRNA" /cultivar="Nagina 22 (indica sub sp)" /db_xref="taxon:39946" /clone="NL_19_92" /tissue_type="Entire leaf tissue" /dev_stage="35 day-old seedlings" /clone_lib="Drought stress (leaf)" /note="Organ: Leaf; Vector: T733pac; ESTs from normalized leaf cDNA library from drought stressed seedlings"			
ORIGIN				
Query Match	3.9%; Score 30; DB 13; Length 577;			
Best Local Similarity	100.0%; Pred. No. 0.091;			
Matches	30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Oy	507 ATATGATATATATATATATATATATGCATT 536			
Db	391 ATATATATATATATATATATATATATTCGATT 420			
RESULT 14				
BUE73763/c				
LOCUS	NL_19_92 Drought stress (leaf) Oryza sativa (indica cultivar-group)			
DEFINITION	cDNA clone NL_19_92 3', mRNA sequence.			
ACCESSION	BUE73763			
KEYWORD	BUE73763.1 GI:23514684			
EST.				
Oryza sativa (indica cultivar-group)				
Oryza sativa (indica cultivar-group)				
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
Spermatophyte; Magnoliophyta; Liliopsida; Poales; Poaceae;				
Ehretoidae; Oryzaceae; Oryza.				
1 (bases 1 to 577)				
Reddy A.R., Marikandeya,G., Ramakrishna,W., Nagabushana,I., Ravindra Babu,P., Madana Mohan Reddy,A., Chandra Sekhar,A. and Benneetzen,J.L.				
Novel EST enrichment with normalized cDNA libraries from drought stressed rice (Oryza sativa L.cv Nagina 22) (2002)				
Unpublished (2002)				
Contact: Reddy AR				
Department of Plant Sciences, School of Life Sciences				
University of Hyderabad				
P.O. Central University, Hyderabad-500 046, A.P, India				
Tel.: 0091-40-3010265				
Fax: 0091-40-3010145				

```

FEATURES
  Source
    Email: arjunsleuohyd.ernet.in
    Insert Length: 577 Std Error: 0.00
    Seq primer: CGCAGGATTTCCACGACGACGAC.
    Location/Qualifiers
      1..577
        /organism="Oryza sativa (indica cultivar-group)"
        /mol_type="mRNA"
        /cultiivar="Nagina 22 (indica sub sp)"
        /db_xref="taxon:39946"
        /clone="NL 19 92"
        /tissue_type="Entire leaf tissue"
        /dev_stage="35 day-old seedlings"
        /clone_id="Drought stress (leaf)"
        /note="Organ: Leaf; Vector: TT73Pac; ESTs from normalized leaf cDNA library from drought stressed seedlings"

ORIGIN
  Query Match 3.9%; Score 30; DB 13; Length 577;
  Best Local Similarity 100.0%; Pred. No. 0.091;
  Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0

  501 AAATCGATATATATATATATATATATATAT 530
      |||||
  420 AAATCGATATATATATATATATATATATAT 392

  RESULT 15
  BI306166
  LOCUS
  DEFINITION
  NL_3_007 Drought stress (leaf) Oryza sativa (indica cultivar-group).
  CDNA clone NL_3_007 3', mRNA sequence.
  BI306166
  BI306166.1 GI:14981488
  EST.
  Oryza sativa (indica cultivar-group)
  Oryza sativa (indica cultivar-group)
  Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
  Ehrhartoideae; Oryzaceae; Oryza.
  1 (bases 1 to 633)
  Reddy, A. R., Rameshkrishna, W., Chandraseekar, A., Nagabushan, I.,
  Ravindrababu, P. and Bernmetzen, J. L.
  Novel EST enrichment with normalized cDNA libraries from drought
  stressed rice (Oryza sativa L cv Nagina 22)
  Unpublished (2001)
  Contact: Reddy AR
  Department of Plant Sciences, School of Life Sciences
  University of Hyderabad
  P. O. Central University, Hyderabad-500 046, A.P., India
  Tel: 0091-40-3010265
  Fax: 0091-40-3010145
  Email: arjunsleuohyd.ernet.in
  Insert Length: 633 Std Error: 0.00
  Plate: 3 row: 3 column: 07
  Seq primer: GTAACGACGCGCACGTC.
  Location/Qualifiers
    1..633
      /organism="Oryza sativa (indica cultivar-group)"
      /mol_type="mRNA"
      /cultiivar="Nagina 22 (indica sub sp)"
      /db_xref="taxon:39946"
      /clone="NL_3_007"
      /tissue_type="Entire leaf tissue"
      /dev_stage="35 day-old seedlings"
      /clone_id="Drought stress (leaf)"
      /note="Organ: Leaf; Vector: TT73Pac; ESTs from normalized leaf cDNA library from drought stressed seedlings"

ORIGIN
  Query Match 3.9%; Score 30; DB 12; Length 633;
  Best Local Similarity 100.0%; Pred. No. 0.086;
  Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0

```

Tue Jul 6 09:07:34 2004

us-10-031-818b-1.oli.rst

Page 7

```

QY      501 AAATCGATATATATATATATATATAT 530
        |||||
Db      109 AAATCGATATATATATATATATATAT 138

```

Search completed: July 5, 2004, 00:57:37
Job time : 2679 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Comphen Ltd.

OK nucleic - nucleic search, using sw model

Run on: July 4, 2004, 22:00:21 ; Search time 82 Seconds
(without alignments)

5204.357 Million cell updates/sec

Title: US-10-031-818b-1

Perfect score: 769
Sequence: 1 gggagctcttcttaataatcc.....ggtagtttgragattcc 769

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 682709 segs, 277475446 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Listing first 45 summaries

Database:

Issued Patents NA: *
1: /cgn2_6/prodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/prodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/prodata/2/ina/5A_COMB.seq:*
4: /cgn2_6/prodata/2/ina/5B_COMB.seq:*
5: /cgn2_6/prodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/prodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	3.5	3528	3	US-08-984-320-2
2	27	3.5	3528	3	US-08-984-320-2
3	27	3.5	3528	3	US-08-984-320-2
4	27	3.5	3528	3	US-08-984-320-2
5	27	3.5	3528	3	US-08-984-320-2
6	27	3.5	3528	3	US-08-984-320-2
7	27	3.5	3528	3	US-08-984-320-2
8	27	3.5	3528	3	US-08-984-320-2
9	27	3.5	3528	3	US-08-984-320-2
10	27	3.5	3528	3	US-08-984-320-2
11	27	3.5	3528	3	US-08-984-320-2
12	27	3.5	3528	3	US-08-984-320-2
13	27	3.5	3528	3	US-08-984-320-2
14	27	3.5	3528	3	US-08-984-320-2
15	27	3.5	3528	3	US-08-984-320-2
16	27	3.5	3528	3	US-08-984-320-2
17	27	3.5	3528	3	US-08-984-320-2
18	27	3.5	3528	3	US-08-984-320-2
19	27	3.5	3528	3	US-08-984-320-2
20	27	3.5	3528	3	US-08-984-320-2
21	27	3.5	3528	3	US-08-984-320-2
22	27	3.5	3528	3	US-08-984-320-2
23	27	3.5	3528	3	US-08-984-320-2
24	27	3.5	3528	3	US-08-984-320-2
25	27	3.5	3528	3	US-08-984-320-2
26	27	3.5	3528	3	US-08-984-320-2
27	27	3.5	3528	3	US-08-984-320-2

28	25	3.3	3395	4	US-09-026-221-3	Sequence 3, Appli
29	25	3.3	5796	4	US-09-366-715-4	Sequence 4, Appli
30	25	3.3	5796	4	US-09-366-715-4	Sequence 4, Appli
31	25	3.3	6550	4	US-09-097-319A-1	Sequence 1, Appli
32	25	3.3	6550	4	US-09-097-319A-1	Sequence 1, Appli
33	25	3.3	6766	4	US-09-527-058-1	Sequence 1, Appli
34	25	3.3	6766	4	US-09-527-058-1	Sequence 1, Appli
35	25	3.3	7560	3	US-09-103-478-4	Sequence 4, Appli
36	25	3.3	7560	3	US-09-103-478-4	Sequence 4, Appli
37	25	3.3	7560	4	US-09-193-931C-4	Sequence 4, Appli
38	25	3.3	7560	4	US-09-193-931C-4	Sequence 4, Appli
39	25	3.3	7560	4	US-09-026-221-4	Sequence 4, Appli
40	25	3.3	7560	4	US-09-026-221-4	Sequence 4, Appli
41	25	3.3	8537	4	US-10-204-708-42	Sequence 42, Appli
42	25	3.3	8537	4	US-10-204-708-42	Sequence 42, Appli
43	25	3.3	9299	4	US-09-097-319A-15	Sequence 15, Appli
44	25	3.3	9299	4	US-09-097-319A-15	Sequence 15, Appli
45	25	3.3	9408	4	US-09-097-319A-16	Sequence 16, Appli

ALIGNMENTS

RESULT 1
US-08-984-320-2
Sequence 2, Application US/08984320
Patent No. 6222097
GENERAL INFORMATION:
APPLICANT: Mcbride, Kevin B.
TITLE OF INVENTION: Use of Ovary-Tissue Transcriptional Factors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSER: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: CA
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1 (a)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/984,320
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/487,087
FILING DATE: 07-JUN-95
APPLICATION NUMBER: USSN 07/998,158
FILING DATE: 29-DEC-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 07/554,195
FILING DATE: 17-JUL-90
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 07/382,518
FILING DATE: 19-JUL-89
ATTORNEY/AGENT INFORMATION:
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
NAME: Carl J. Schmedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CGNE 91-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3528 base pairs
TYPE: nucleic acid
STRANDEDNESS: double

Page 2

507 ATATATATATATATATATATCGA 533

```

; TITLE OF INVENTION: Use of Ovary-Tissue Transcriptional Factors
; NUMBER OF SEQUENCES: 6

```

```

CORRESPONDENCE ADDRESS:
ADDRESS: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: CA
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1 (a)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,087A
FILING DATE: 07-JUN-95
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 07/998,158
FILING DATE: 29-DEC-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 07/554,195
FILING DATE: 17-JUL-90
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 07/382,518
FILING DATE: 19-JUL-89
ATTORNEY/AGENT INFORMATION:
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
REFERENCE/DOCKET NUMBER: CGNE 91-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3528 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
US-08-487-087A-2

Query Match
Best Local Similarity 3.5%; Score 27; DB 3; Length 3528;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 507 ATATATATATATATATATATCGA 533
DB 2413 ATATATATATATATATATATCGA 2387

RESULT 5
US-08-397-653B-2
Sequence 2, Application US/08397653B
Patent No. 6329570
GENERAL INFORMATION:
APPLICANT: Martineau, Belinda
TITLE OF INVENTION: COTTON MODIFICATION USING
TITLE OF INVENTION: OVARY-TISSUE TRANSCRIPTIONAL
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESS: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: CA
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
```

```

SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,653B
FILING DATE: 28-FEB-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Lassen
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CGNE 112
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4383 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
US-08-397-653B-2

Query Match
Best Local Similarity 3.5%; Score 27; DB 4; Length 4383;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 504 TCGATATATATATATATATATATAT 530
DB 2387 TCGATATATATATATATATATATAT 2413

RESULT 6
US-08-397-653B-2/c
Sequence 2, Application US/08397653B
Patent No. 6329570
GENERAL INFORMATION:
APPLICANT: Martineau, Belinda
TITLE OF INVENTION: COTTON MODIFICATION USING
TITLE OF INVENTION: OVARY-TISSUE TRANSCRIPTIONAL
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESS: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: CA
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.0
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,653B
FILING DATE: 28-FEB-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Lassen
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CGNE 112
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
```

LENGTH: 4383 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
US-08-397-653B-2

Query Match 3.5%: Score 27; DB 4; Length 4383;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 507 ATATATATATATATATATATATCGA 533
DB 2413 ATATATATATATATATATATATCGA 2387

RESULT 7
5175095-4

Patent No. 5175095
APPLICANT: Martineau, Belinda M.; Houck, Catherine M.
TITLE OF INVENTION: OVARY TISSUE TRANSCRIPTIONAL FACTORS
NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/554,195
FILING DATE: 17-JUL-1990
SEQ ID NO: 4
LENGTH: 4383

Query Match 3.5%: Score 27; DB 6; Length 4383;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 504 TCGATATATATATATATATATATAT 530
DB 2387 TCGATATATATATATATATATATAT 2413

RESULT 8
5175095-4/C

Patent No. 5175095
APPLICANT: Martineau, Belinda M.; Houck, Catherine M.
TITLE OF INVENTION: OVARY TISSUE TRANSCRIPTIONAL FACTORS
NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/554,195
FILING DATE: 17-JUL-1990
SEQ ID NO: 4
LENGTH: 4383

Query Match 3.5%: Score 27; DB 6; Length 4383;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 507 ATATATATATATATATATATATCGA 533
DB 2413 ATATATATATATATATATATATCGA 2387

RESULT 9
5177307-1

Patent No. 5177307
APPLICANT: HOUCK, CATHERINE M.; PEAR, JULIE R.; MARTINEAU, BELINDA M.; HIATT, WILLIAM
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATIONS OF ENDOGENOUS CYTOKININ LEVELS
NUMBER OF SEQUENCES: 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/554,196
FILING DATE: 17-JUL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 382,802

FILING DATE: 19-JUL-1989
APPLICATION NUMBER: 188,361
FILING DATE: 29-APR-1988
APPLICATION NUMBER: 168,190
FILING DATE: 15-MAR-1988
APPLICATION NUMBER: 54,369
FILING DATE: 26-MAY-1987
SEQ ID NO: 1
LENGTH: 4383
5177307-1

Query Match 3.5%: Score 27; DB 6; Length 4383;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 504 TCGATATATATATATATATATATAT 530
DB 2387 TCGATATATATATATATATATATAT 2413

RESULT 10
5177307-1/C

Patent No. 5177307
APPLICANT: HOUCK, CATHERINE M.; PEAR, JULIE R.; MARTINEAU, BELINDA M.; HIATT, WILLIAM
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATIONS OF ENDOGENOUS CYTOKININ LEVELS
NUMBER OF SEQUENCES: 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/554,196
FILING DATE: 17-JUL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 382,802
FILING DATE: 19-JUL-1989
APPLICATION NUMBER: 188,361
FILING DATE: 29-APR-1988
APPLICATION NUMBER: 168,190
FILING DATE: 15-MAR-1988
APPLICATION NUMBER: 54,369
FILING DATE: 26-MAY-1987
SEQ ID NO: 1
LENGTH: 4383
5177307-1

Query Match 3.5%: Score 27; DB 6; Length 4383;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 507 ATATATATATATATATATATATCGA 533
DB 2413 ATATATATATATATATATATATCGA 2387

RESULT 11
US-09-451-651-34

Sequence 34, Application US/09451651
Patent No. 6489101
GENERAL INFORMATION:
APPLICANT: DILLON, DAVID CLIFFORD
APPLICANT: DAY, CRAIG HILTING
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND DIAGNOSIS
FILE REFERENCE: 210121.491
CURRENT APPLICATION NUMBER: US/09/451,651
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 34
LENGTH: 432
TYPE: DNA
ORGANISM: Homo sapiens
US-09-451-651-34

Db 799 ATATATATATATATATATATATATC 775

RESULT 15

US-09-171-209-20

; Sequence 20; Application US/09171209

; Patent No. 644800

; GENERAL INFORMATION:

; APPLICANT: VANDERBILT UNIVERSITY

; 305 Kirkland Hall

; Nashville, TN 37240

; TITLE OF INVENTION: MAMMALIAN GENES INVOLVED IN VIRAL

; INFECTION

; NUMBER OF SEQUENCES: 83

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Needle & Rosenberg, P.C.

; STREET: 127 Peachtree Street, Suite 1200

; CITY: Atlanta

; STATE: Georgia

; COUNTRY: USA

; ZIP: 30303-1811

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/171,209

; FILING DATE: 08-Mar-1999

; CLASSIFICATION: <unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US97/06067

; FILING DATE: <unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Selby, Elizabeth

; REGISTRATION NUMBER: 38,298

; REFERENCE/DOCKET NUMBER: 22000.0061/P

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 404 688 0770

; TELEFAX: 404 688 9880

; INFORMATION FOR SEQ ID NO: 20:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 888 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; SEQUENCE DESCRIPTION: SEQ ID NO: 20:

US-09-171-209-20

Query Match 3.3%; Score 25; DB 4; Length 888;

Best Local Similarity 100.0%; Pred. No. 0.054;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 506 GATATATATATATATATATATAT 530

Db 780 GATATATATATATATATATATAT 804

Search completed: July 4, 2004, 23:16:01
Job time : 83 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Comphen Ltd.

CM nucleic - nucleic search, using sw model

Run on: July 4, 2004, 23:16:07 ; Search time 445 Seconds
(without alignments)
8336.664 Million cell updates/sec

Title: US-10-031-818b-1

Sequence: 1 999atcttttaaaataacc.....gtagctttagattcc 769

Scoring table: OLIGO NUC
Gapop 60.0, Gapext 60.0

Searched: 3163042 seqs, 2412103800 residues

Word size: 0

Total number of hits satisfying chosen parameters: 6326084

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: Published Applications NA.*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
3: /cgn2_6/ptodata/2/pubpna/US05_PUBCOMB.seq.*
4: /cgn2_6/ptodata/2/pubpna/US04_PUBCOMB.seq.*
5: /cgn2_6/ptodata/2/pubpna/US03_PUBCOMB.seq.*
6: /cgn2_6/ptodata/2/pubpna/US02_PUBCOMB.seq.*
7: /cgn2_6/ptodata/2/pubpna/US01_PUBCOMB.seq.*
8: /cgn2_6/ptodata/2/pubpna/US00_PUBCOMB.seq.*
9: /cgn2_6/ptodata/2/pubpna/US99_PUBCOMB.seq.*
10: /cgn2_6/ptodata/2/pubpna/US98_PUBCOMB.seq.*
11: /cgn2_6/ptodata/2/pubpna/US97_PUBCOMB.seq.*
12: /cgn2_6/ptodata/2/pubpna/US96_PUBCOMB.seq.*
13: /cgn2_6/ptodata/2/pubpna/US95_PUBCOMB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US94_PUBCOMB.seq.*
15: /cgn2_6/ptodata/2/pubpna/US93_PUBCOMB.seq.*
16: /cgn2_6/ptodata/2/pubpna/US92_PUBCOMB.seq.*
17: /cgn2_6/ptodata/2/pubpna/US91_PUBCOMB.seq.*
18: /cgn2_6/ptodata/2/pubpna/US90_PUBCOMB.seq.*
19: /cgn2_6/ptodata/2/pubpna/US89_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	3.5	3528	9	US-09-777-347-2
2	27	3.5	3528	9	US-09-777-347-2
3	27	3.5	6526	15	US-10-311-455-2209
4	27	3.5	6526	15	US-10-311-455-2209
5	26	3.4	207	17	US-10-437-963-79690
6	26	3.4	207	17	US-10-437-963-79690
7	26	3.4	404	13	US-10-424-599-60831
8	26	3.4	404	13	US-10-424-599-60831
9	26	3.4	419	13	US-10-424-599-100147
10	26	3.4	419	13	US-10-424-599-100147
11	26	3.4	440	13	US-10-424-599-95178
12	26	3.4	440	13	US-10-424-599-95178
13	26	3.4	506	17	US-10-437-963-94087
14	26	3.4	506	17	US-10-437-963-94087

15	26	3.4	549	10	US-09-991-936-1818	Sequence 1818, Ap
16	26	3.4	549	10	US-09-991-936-1818	Sequence 1818, Ap
17	26	3.4	623	17	US-10-437-963-61122	Sequence 61122, A
18	26	3.4	623	17	US-10-437-963-61122	Sequence 61122, A
19	26	3.4	1079	17	US-10-437-963-80924	Sequence 80924, A
20	26	3.4	1079	17	US-10-437-963-80924	Sequence 80924, A
21	26	3.4	1218	17	US-10-437-963-92758	Sequence 92758, A
22	26	3.4	1218	17	US-10-437-963-92758	Sequence 92758, A
23	26	3.4	1461	9	US-09-938-842A-3207	Sequence 3207, Ap
24	26	3.4	1461	9	US-09-938-842A-3207	Sequence 3207, Ap
25	26	3.4	1461	11	US-09-938-842A-3207	Sequence 3207, Ap
26	26	3.4	1461	11	US-09-938-842A-3207	Sequence 3207, Ap
27	26	3.4	2000	9	US-09-938-842A-2951	Sequence 2951, Ap
28	26	3.4	2000	9	US-09-938-842A-2951	Sequence 2951, Ap
29	26	3.4	2000	9	US-09-938-842A-4203	Sequence 4203, Ap
30	26	3.4	2000	9	US-09-938-842A-4203	Sequence 4203, Ap
31	26	3.4	2000	11	US-09-938-842A-2951	Sequence 2951, Ap
32	26	3.4	2000	11	US-09-938-842A-2951	Sequence 2951, Ap
33	26	3.4	2000	11	US-09-938-842A-4203	Sequence 4203, Ap
34	26	3.4	2000	11	US-09-938-842A-4203	Sequence 4203, Ap
35	26	3.4	3559	13	US-08-892-635A-18	Sequence 18, Appl
36	26	3.4	3559	13	US-08-892-635A-18	Sequence 18, Appl
37	26	3.4	24023	14	US-10-094-679-1	Sequence 1, Appl1
38	26	3.4	24023	14	US-10-094-679-1	Sequence 1, Appl1
39	26	3.4	33675	9	US-09-921-992-2	Sequence 2, Appl1
40	26	3.4	33675	9	US-09-921-992-2	Sequence 2, Appl1
41	26	3.4	330973	13	US-10-087-192-1498	Sequence 1498, Ap
42	26	3.4	330973	13	US-10-087-192-1498	Sequence 1498, Ap
43	26	3.4	1503841	9	US-09-795-668-1	Sequence 1, Appl1
44	26	3.4	1503841	9	US-09-795-668-1	Sequence 1, Appl1
45	26	3.4	1503841	9	US-09-795-668-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-09-777-347-2
Sequence 2, Application US/09777347
Parent No. US20010014977A1
GENERAL INFORMATION:
APPLICANT: McBride, Kevin E.
TITLE OF INVENTION: Use of Ovary-Tissue Transcriptional Factors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESS: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: CA
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1 (a)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/777,347
FILING DATE: 05-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,087
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 07/554,195
FILING DATE: 17-JUL-90
APPLICATION NUMBER: USSN 07/382,518
FILING DATE: 19-JUL-89
ATTORNEY/AGENT INFORMATION:
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CGNE 91-1
TELECOMMUNICATION INFORMATION:

TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 3528 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 2
US-09-777-347-2

Query Match 3.5%; Score 27; DB 9; Length 3528;
Best Local Similarity 100.0%; Pred. No. 0.058; 0; Indels 0; Gaps 0;
Matches 27; Conservative 0; Mismatches 0;

QY 504 TCGATATATATATATATATATATAT 530
DB 2387 TCGATATATATATATATATATATAT 2413

RESULT 2
US-09-777-347-2/c
Sequence 2, Application US/09777347
Patent No. US2001001497A1
GENERAL INFORMATION:
APPLICANT: MCBride, Kevin E.
TITLE OF INVENTION: Use of Ovary-Tissue Transcriptional Factors
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: CA
COUNTRY: USA
ZIP: 95616

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.3 (a)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/777,347
FILING DATE: 05-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,087
FILING DATE: <Unknown>
APPLICATION NUMBER: USSN 07/554,195
FILING DATE: 17-JUL-90
APPLICATION NUMBER: USSN 07/382,518
FILING DATE: 19-JUL-89
ATTORNEY/AGENT INFORMATION:
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CGNE 91-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 3528 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 2
US-09-777-347-2

Query Match 3.5%; Score 27; DB 9; Length 3528;
Best Local Similarity 100.0%; Pred. No. 0.058; 0; Indels 0; Gaps 0;
Matches 27; Conservative 0; Mismatches 0;

QY 507 ATATATATATATATATATATATATCGA 533
DB 2413 ATATATATATATATATATATATCGA 2387

RESULT 3
US-10-311-455-2209
Sequence 2209, Application US/10311455
Publication No. US20030143606A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Det
TITLE OF INVENTION: Cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 2209
LENGTH: 6526
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-2209

Query Match 3.5%; Score 27; DB 15; Length 6526;
Best Local Similarity 100.0%; Pred. No. 0.062; 0; Indels 0; Gaps 0;
Matches 27; Conservative 0; Mismatches 0;

QY 504 TCGATATATATATATATATATATATAT 530
DB 3500 TCGATATATATATATATATATATAT 3526

RESULT 4
US-10-311-455-2209/c
Sequence 2209, Application US/10311455
Publication No. US20030143606A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Det
TITLE OF INVENTION: Cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 2209
LENGTH: 6526
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-2209

Query Match 3.5%; Score 27; DB 15; Length 6526;
Best Local Similarity 100.0%; Pred. No. 0.062; 0; Indels 0; Gaps 0;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 507 ATATATATATATATATATATATCGA 533
|||||
DB 3526 ATATATATATATATATATATATCGA 3500

RESULT 5
US-10-437-963-79690
; Sequence 79690, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Soukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 79690
; LENGTH: 207
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_79386C.1
US-10-437-963-79690

Query Match 3.4%; Score 26; DB 17; Length 207;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 507 ATATATATATATATATATATCG 532
|||||
DB 10 ATATATATATATATATATATATCG 35

RESULT 6
US-10-437-963-79690/c
; Sequence 79690, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Soukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 79690
; LENGTH: 207
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_79386C.1
US-10-437-963-79690

Query Match 3.4%; Score 26; DB 17; Length 207;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 505 CGATATATATATATATATATAT 530
|||||
DB 35 CGATATATATATATATATATATAT 10

RESULT 7
US-10-424-599-60831
; Sequence 60831, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 60831
; LENGTH: 404
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_25943C.1
US-10-424-599-60831

Query Match 3.4%; Score 26; DB 13; Length 404;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 505 CGATATATATATATATATATAT 530
|||||
DB 11 CGATATATATATATATATATATAT 36

RESULT 8
US-10-424-599-60831/c
; Sequence 60831, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 60831
; LENGTH: 404
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_25943C.1
US-10-424-599-60831

Query Match 3.4%; Score 26; DB 13; Length 404;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 507 ATATATATATATATATATATATCG 532
|||||
DB 36 ATATATATATATATATATATATCG 11

RESULT 9
US-10-424-599-100147
; Sequence 100147, Application US/10424599

```
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 100147
LENGTH: 419
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_61448C.1
US-10-424-599-100147
```

```
Query Match          3.4%; Score 26; DB 13; Length 419;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Cy 505 CGATATATATATATATATATATAT 530
Db 62 CGATATATATATATATATATATAT 87
```

```
RESULT 10
US-10-424-599-100147/C
Sequence 100147, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 100147
LENGTH: 419
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_61448C.1
US-10-424-599-100147
```

```
Query Match          3.4%; Score 26; DB 13; Length 419;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Cy 507 ATATATATATATATATATATATATCG 532
Db 87 ATATATATATATATATATATATATCG 62
```

```
RESULT 11
US-10-424-599-95178
Sequence 95178, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
```

```
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 95178
LENGTH: 440
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_56959C.1
US-10-424-599-95178
```

```
Query Match          3.4%; Score 26; DB 13; Length 440;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Cy 505 CGATATATATATATATATATATAT 530
Db 11 CGATATATATATATATATATATAT 36
```

```
RESULT 12
US-10-424-599-95178/C
Sequence 95178, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 95178
LENGTH: 440
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_56959C.1
US-10-424-599-95178
```

```
Query Match          3.4%; Score 26; DB 13; Length 440;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Cy 507 ATATATATATATATATATATATATCG 532
Db 36 ATATATATATATATATATATATATCG 11
```

```
RESULT 13
US-10-437-963-94087
Sequence 94087, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 94087
LENGTH: 506
```

Tue Jul 6 09:07:33 2004

us-10-031-818b-1.011.rnpb

Page 5

TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_92409C.1
US-10-437-963-94087

Query Match 3.4%; Score 26; DB 17; Length 506;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 507 ATATATATATATATATATATATCG 532
DB 34 ATATATATATATATATATATATCG 59

RESULT 14
US-10-437-963-94087/C
Sequence 94087, Application US/10437963
Publication No. US2004012343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukhartov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 94087
LENGTH: 506
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_92409C.1
US-10-437-963-94087

Query Match 3.4%; Score 26; DB 17; Length 506;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 505 CGATATATATATATATATATATAT 530
DB 59 CGATATATATATATATATATATAT 34

RESULT 15
US-09-991-936-1818
Sequence 1818, Application US/09991936
Publication No. US20030073827A1
GENERAL INFORMATION:
APPLICANT: Brandt, Kevin S.
APPLICANT: Gaines, Patrick J.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Wisniewski, Nancy
TITLE OF INVENTION: FLEA HEAD, NERVE CORD, HINDGUT AND MALPIGHIAN TUBULE
TITLE OF INVENTION: NUCLEIC ACID MOLECULES, PROTEINS AND USES THEREOF
FILE REFERENCE: FC-6-C1
CURRENT APPLICATION NUMBER: US/09/991,936
CURRENT FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US/09/543,668
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 60/128,704
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 1959
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1818
LENGTH: 549

TYPE: DNA
ORGANISM: Ctenocephalides felis
US-09-991-936-1818

Query Match 3.4%; Score 26; DB 10; Length 549;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 507 ATATATATATATATATATATATCG 532
DB 491 ATATATATATATATATATATATCG 516

Search completed: July 5, 2004, 01:09:04
Job time : 448 secs